

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:05:45 ; Search time 364.655 Seconds

(without alignments)
5985.683 Million cell updates/sec

Title: US-08-935-377-3

Sequence: 1 GGCCAAATTTGAATTTA.....GCCCGCCGCCAAGCGCGA 75

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_ph:*
7: gb_pl:*
8: gb_pr:*
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13: gb_vl:*
14: em_ba:*
15: em_fun:*
16: em_hum:*
17: em_in:*
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19: em_om:*
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21: em_ov:*
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23: em_ph:*
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25: em_ro:*
26: em_sts:*
27: em_un:*
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29: em_htg_hum:*
30: em_htg_inv:*
31: em_htg_other:*
32: em_htg_mus:*
33: em_htg_pin:*
34: em_htg_rod:*
35: em_htg_mam:*
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37: em_sy:*
38: em_htgo_hum:*
39: em_htgo_mus:*
40: em_htgo_other:*
41: em_htgo_hum:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	75	100.0	75	6	AX326742	AX326742 Sequence
2	59	78.7	59	6	AX326760	AX326760 Sequence
3	59	78.7	59	6	AX326761	AX326761 Sequence
4	42.4	56.5	77	6	AX326768	AX326768 Sequence
5	40.6	54.1	2164	14	VH3FDPCL	X89856 V. virus DNA
6	40.6	54.1	2164	14	VH3FDPCL	X89857 V. virus DNA
7	40	53.3	84	6	A59039	A59039 Sequence 27
8	40	53.3	86	6	A59040	A59040 Sequence 28
9	39.6	53.1	78	6	AX007101	AX007101 Sequence
10	39.6	52.8	6474	6	AR105797	AR105797 Sequence
11	38.8	51.7	78	6	AX007102	AX007102 Sequence
12	38.8	51.7	5532	6	AR105803	AR105803 Sequence
13	38.4	51.2	49	6	AR105801	AR105801 Sequence
14	38.4	51.2	77	6	AX326769	AX326769 Sequence
15	38.4	51.2	6811	6	AR105798	AR105798 Sequence
16	38.2	50.9	139	6	AX003203	AX003203 Sequence
17	38.2	50.9	7252	6	AR176235	AR176235 Sequence
18	38.2	50.9	7252	6	AX003206	AR176236 Sequence
19	38.2	50.9	7387	6	AR176236	AX003207 Sequence
20	38.2	50.9	7387	6	AX003207	AX007114 Sequence
21	38	50.7	41	6	AX007114	AR105787 Sequence
22	38	50.7	51	6	AR105787	AR105788 Sequence
23	38	50.7	53	6	AR105788	AR105796 Sequence
24	38	50.7	53	6	AR105796	AX326740 Sequence
25	37	49.3	69	6	AX326740	AC100784 Homo sapi
26	37	49.3	69	6	AX326740	AC027018 Homo sapi
27	33	44.0	173811	9	AC100784	AC097416 Rattus no
28	32.2	42.9	242336	2	AC097416	AC095070 Rattus no
29	32	42.7	148730	2	AC095070	AC079849 Homo sapi
30	31.8	42.4	161695	2	AC079849	AC078826 Homo sapi
31	31.8	42.4	187052	2	AC078826	AC020612 Homo sapi
32	31.8	42.4	187052	2	AC020612	AC009246 Homo sapi
33	31.8	42.4	188928	9	AC020612	AC108271 Rattus no
34	31.8	42.4	266033	2	AC108271	AC101893 Mus muscu
35	31.4	41.9	158356	2	AC101893	AC097553 Rattus no
36	31.2	41.6	147361	2	AC097553	AC094078 Rattus no
37	31.2	41.6	162143	2	AC094078	LI3028 Mouse inter
38	31.2	41.6	165563	2	AC094078	AL645741 Mouse DNA
39	31	41.3	4376	10	MUSIL13A	AC126191 Rattus no
40	31	41.3	121121	10	AL645741	AC084392 Mus muscu
41	31	41.3	138293	2	AC126191	AC126645 Rattus no
42	31	41.3	142732	10	AC084392	AC005742 Mus muscu
43	31	41.3	159314	2	AC126645	AC020886 Mus muscu
44	31	41.3	159500	10	AC005742	
45	31	41.3	237823	2	AC020886	

ALIGNMENTS

RESULT 1
AX326742
LOCUS AX326742 75 bp DNA Linear PAT 07-JAN-2002
DEFINITION Sequence 3 from Patent WO0172955.
ACCESSION AX326742
VERSION AX326742.1 GI:18097468
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
REFERENCE
1 Zauderer,M. and Smith,E.S.
AUTHORS Methods of producing a library and methods of selecting
TITLE Polynucleotides of interest
JOURNAL Patent: WO 01/72955-A 3 04-OCR-2001;

UNIVERSITY OF ROCHESTER (US)
Location/Qualifiers
1..75
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Nucleotide Sequence of pEL/tk"

BASE COUNT 19 a 16 c 19 g 21 t

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Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCAAAATGAAATTTATTTTGGAAATATAAAGCGCCGCATGGCCGC 60
Db 1 GCCCAAAATGAAATTTATTTTGGAAATATAAAGCGCCGCATGGCCGC 60

Qy 61 GCCGCCAAGCGCGGA 75
Db 61 GCCGCCAAGCGCGGA 75

RESULT 2
LOCUS AX326760 59 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 21 from Patent W00172995.
ACCESSION AX326760
VERSION AX326760.1 GI:18097479
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 Zauderer, M. and Smith, E.S.
TITLE Methods of producing a library and methods of selecting
JOURNAL polynucleotides of interest
UNIVERSITY OF ROCHESTER (US)
Patent: WO 0172995-A 21 04-OCT-2001;
Location/Qualifiers

FEATURES
source 1..59
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic EL promoter MM438"

BASE COUNT 16 a 10 c 12 g 21 t

Query Match 78.7%; Score 59; DB 6; Length 59;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCAAAATGAAATTTATTTTGGAAATATAAAGCGCCGCATGGCCGC 59
Db 1 GCCCAAAATGAAATTTATTTTGGAAATATAAAGCGCCGCATGGCCGC 59

RESULT 3
LOCUS AX326761 59 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 22 from Patent W00172995.
ACCESSION AX326761
VERSION AX326761.1 GI:18097480
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 Zauderer, M. and Smith, E.S.
TITLE Methods of producing a library and methods of selecting
JOURNAL polynucleotides of interest
UNIVERSITY OF ROCHESTER (US)
Patent: WO 0172995-A 22 04-OCT-2001;
Location/Qualifiers

FEATURES
source 1..59

/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic EL promoter MM439"

BASE COUNT 21 a 12 c 10 g 16 t

Query Match 78.7%; Score 59; DB 6; Length 59;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AAAAATGAAATTTATTTTGGAAATATAAAGCGCCGCATGGCCGC 63
Db 59 AAAAATGAAATTTATTTTGGAAATATAAAGCGCCGCATGGCCGC 1

RESULT 4
LOCUS AX326768 77 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 29 from Patent W00172995.
ACCESSION AX326768
VERSION AX326768.1 GI:18097486
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 Zauderer, M. and Smith, E.S.
TITLE Methods of producing a library and methods of selecting
JOURNAL polynucleotides of interest
UNIVERSITY OF ROCHESTER (US)
Patent: WO 0172995-A 29 04-OCT-2001;
Location/Qualifiers

FEATURES
source 1..77
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Elova"

BASE COUNT 29 a 7 c 11 g 30 t

Query Match 56.5%; Score 42.4; DB 6; Length 77;
Best Local Similarity 97.7%; Pred. No. 0.011;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCAAAATGAAATTTATTTTGGAAATATAAAGCGCCGCATGGCCGC 44
Db 1 GCCCAAAATGAAATTTATTTTGGAAATATAAAGCGCCGCATGGCCGC 44

RESULT 5
LOCUS VWH3FDPCL 2164 bp DNA linear VRL 03-JAN-1996
DEFINITION V. virus DNA for Hind III F fragment (clone VDPCL).
ACCESSION X89856
VERSION X89856.1 GI:927568
KEYWORDS HindIII F fragment; hph gene; hygromycin phosphotransferase;
promoter.
SOURCE Vaccinia virus.
ORGANISM Vaccinia virus.
REFERENCE 1 (bases 1 to 2164)
AUTHORS Pfliegerer, M., Falkner, F.G. and Dörner, F.
TITLE A novel vaccinia virus expression system allowing construction of
recombinants without the need for selection markers, plasmids and
bacterial hosts
JOURNAL J. Gen. Virol. 76 (Pt 12), 2957-2962 (1995)
MEDLINE 96112180
PUBMED 8847500
REFERENCE 2 (bases 1 to 2164)
AUTHORS Pfliegerer, M.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-1995) M. Pfliegerer, Immuno AG, A. 2304
Orth/Donau, Uferstrasse 15, AUSTRIA

```

COMMENT      Related sequence M35027.
FEATURES
  Source      Location/Qualifiers
              1..2164
                /organism="Vaccinia virus"
                /strain="WR"
                /specific_host="mammalians"
                /db_xref="taxon:10245"
                /map="45478 nt number"
                /clone="VDPc 1"
                /cell_line="recombinant Vaccinia virus"
                /lab_host="mammalian cell lines"
  misc_feature 1..485
    /note="Hind III F fragment"
  misc_feature 479..1662
    /note="NOT I gene cassette"
  misc_feature 479
    /note="NOT I cleavage site corresponding to the unique NOT
    I site in the Vv genome at position 45478 (strain
    Copenhagen)"
  promoter      486..543
    /note="strong synthetic early/late promoter"
  misc_feature 536
    /note="unique sfi I cleavage site"
  promoter      544..594
    /note="weak synthetic early/late promoter"
  gene          595..1620
    /gene="hph"
    /gene="hph"
    /gene="hph"
  CDS           595..1620
    /gene="hph"
    /codon_start=1
    /product="hygromycin phosphotransferase"
    /protein_id="CAA61952.1"
    /db_xref="GI:953210"
    /translation="MKKPELTATSVKFLIEKFDVSVDLMQISEGESRAFSFDVGR
    GYLRVNSCADGFYKDRVYRHFASALPIPEVLDIGEFSESLTICISRAAGVTLDD
    LPETELPAVLQPVAEAMDAIAADLSOTSGFGPGGICGTYTTRDFICAIADPHY
    HMOTVMDTVASASVAQALDELMADCEPFRHLYHADFGSNVLTIDNGRTIAYIDS
    EMFQDSQYEVANIFFWRPWLACMEQOTRFERRHPELAGSPRLRAYMLRTIGLDLYQ
    SLVDGNFDDAAMAAGRCDAIVRSAGTGVGTQIARRSAVAWTDGCEVLADSGNRRPS
    TRPRAKE"
  misc_feature 1635
    /note="Rsr II cleavage site"
  misc_feature 1642
    /note="NOT I cleavage site"
  misc_feature 1643..2164
    /note="Hind III F fragment"
  BASE COUNT  586 a 488 c 475 g 615 t
  ORIGIN
    Query Match      54.1%; Score 40.6; DB 14; Length 2164;
    Best Local Similarity 73.2%; Pred. No. 0.061;
    Matches 52; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Oy 5 AAAAATTGAATTTATTTTGGAAATATAAGCGCGCCCATGGCCCGCGCG 64
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Db 488 AAAAATTGAATTTATTTTGGAAATATAAGCGCGCGCATATG 547

Oy 65 CCACGCGCGA 75
    |||||
Db 548 TAAAGTTGAA 558

RESULT 6
VH3FDPc2/c 2164 bp DNA linear VRL 03-JAN-1996
LOCUS V.virus DNA for Hind III F fragment (clone VDPc2).
ACCESSION X89857
VERSION X89857.1 GI:927569
KEYWORDS HindIII F fragment; hph gene; hygromycin phosphotransferase;
promoter.
SOURCE Vaccinia virus.
ORGANISM Vaccinia virus.

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REFERENCE
  AUTHORS      1 (bases 1 to 2164)
  TITLE        Pfleiderer, M., Falkner, F.G. and Dörner, F.
  JOURNAL      A novel Vaccinia virus expression system allowing construction of
  MEDLINE      recombinants without the need for selection markers, plasmids and
  PUBMED       bacterial hosts
  96112180
  JOURNAL      J. Gen. Virol. 76 (Pt 12), 2957-2962 (1995)
  MEDLINE      8847500
  PUBMED       2 (bases 1 to 2164)
  JOURNAL      Pfleiderer, M.
  TITLE        Direct Submission
  JOURNAL      Submitted (20-JUL-1995) M. Pfleiderer, Immuno AG, A. 2304
  ORTH/Donau, Uferstrasse 15, AUSTRIA
  COMMENT      Submitted (20-JUL-1995) M. Pfleiderer, Immuno AG, A. 2304
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    Location/Qualifiers
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        /organism="Vaccinia virus"
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        /specific_host="mammalians"
        /db_xref="taxon:10245"
        /map="45478 nt number"
        /clone="VDPc 2"
        /cell_line="recombinant Vaccinia virus"
        /lab_host="Mammalian cell lines"
        1..485
        /note="Hind III F fragment"
        /complement(479..1642)
        /note="NOT I gene cassette"
        479
        /note="NOT I cleavage site corresponding to the unique NOT I
        site in the Vv genome at position 45478 (strain
        Copenhagen)"
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        /complement(506..1531)
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        /codon_start=1
        /product="hygromycin phosphotransferase"
        /protein_id="CAA61953.1"
        /db_xref="GI:953211"
        /translation="MKKPELTATSVKFLIEKFDVSVDLMQISEGESRAFSFDVGR
        GYLRVNSCADGFYKDRVYRHFASALPIPEVLDIGEFSESLTICISRAAGVTLDD
        LPETELPAVLQPVAEAMDAIAADLSOTSGFGPGGICGTYTTRDFICAIADPHY
        HMOTVMDTVASASVAQALDELMADCEPFRHLYHADFGSNVLTIDNGRTIAYIDS
        EMFQDSQYEVANIFFWRPWLACMEQOTRFERRHPELAGSPRLRAYMLRTIGLDLYQ
        SLVDGNFDDAAMAAGRCDAIVRSAGTGVGTQIARRSAVAWTDGCEVLADSGNRRPS
        TRPRAKE"
        complement(1532..1585)
        /note="weak synthetic early/late promoter"
        1592
        /note="Sfi cleavage site"
        /complement(1598..1639)
        /note="strong synthetic early/late promoter"
        1642
        /note="NOT I cleavage site"
        1643..2164
        /note="Hind III F fragment"
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    Query Match      54.1%; Score 40.6; DB 14; Length 2164;
    Best Local Similarity 73.2%; Pred. No. 0.061;
    Matches 52; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Oy 5 AAAAATTGAATTTATTTTGGAAATATAAGCGCGCGCATATG 64
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Db 1638 AAAAATTGAATTTATTTTGGAAATATAAGCGCGCGCATATG 1579

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Viruses: dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

QY 65 CCACGCGCGA 75
 DB 1578 TAAAGTTGAA 1568

RESULT 7
 A59039
 LOCUS A59039 84 bp DNA linear PAT 06-MAR-1998
 DEFINITION Sequence 27 from Patent EP0753581.
 ACCESSION A59039
 VERSION A59039.1 GI:3714474
 KEYWORDS
 SOURCE
 ORGANISM
 unclassified.
 unclassified.
 unclassified.
 1 (bases 1 to 84)
 Scheiflinger, F.D., Antoine, G.D., Falkner, Falko-Guenther, D.,
 Dorner, F.P. and Eibl, J.D.
 Improved recombinant eukaryotic cytoplasmic viruses, method for
 their production and their use as vaccines
 Patent: EP 0753581-A 27 15-JAN-1997;
 IMMUNO AG (AT)

FEATURES
 source
 1. .84
 /organism="unclassified"
 /db_xref="taxon:32644"

BASE COUNT 28 a 8 c 10 g 38 t
 ORIGIN

Query Match 53.3%; Score 40; DB 6; Length 84;
 Best Local Similarity 82.1%; Pred. No. 0.059;
 Matches 46; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 CCAAAATGAAATTTATTTTGGATATATAAGCGCGCCATGGGCC 58
 DB 9 CTTAAATGAAATTTATTTTGGATATATAAGCGCCATGGGCC 64

RESULT 8
 A59040
 LOCUS A59040 86 bp DNA linear PAT 06-MAR-1998
 DEFINITION Sequence 28 from Patent EP0753581.
 ACCESSION A59040
 VERSION A59040.1 GI:3714475
 KEYWORDS
 SOURCE
 ORGANISM
 unclassified.
 unclassified.
 unclassified.
 1 (bases 1 to 86)
 Scheiflinger, F.D., Antoine, G.D., Falkner, Falko-Guenther, D.,
 Dorner, F.P. and Eibl, J.D.
 Improved recombinant eukaryotic cytoplasmic viruses, method for
 their production and their use as vaccines
 Patent: EP 0753581-A 28 15-JAN-1997;
 IMMUNO AG (AT)

FEATURES
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 1. .86
 /organism="unclassified"
 /db_xref="taxon:32644"

BASE COUNT 38 a 11 c 9 g 28 t
 ORIGIN

Query Match 53.3%; Score 40; DB 6; Length 86;
 Best Local Similarity 82.1%; Pred. No. 0.059;
 Matches 46; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 CCAAAATGAAATTTATTTTGGATATATAAGCGCGCCATGGGCC 58
 DB 80 CTTAAATGAAATTTATTTTGGATATATAAGCGCCATGGGCC 25

RESULT 9
 AX007101/c

LOCUS AX007101 78 bp DNA linear PAT 06-SEP-2000
 DEFINITION Sequence 1 from Patent EP0972840.
 ACCESSION AX007101
 VERSION AX007101.1 GI:9994992
 KEYWORDS
 SOURCE
 ORGANISM
 synthetic construct.
 synthetic construct.
 artificial sequences.
 1 (bases 1 to 78)
 Barcena, D.R., Parra, F.F., Blasco, L.R., Morales, C.M., Pages, M.A.,
 Sanchez, V.U., Torres, T.U. and Vazquez, R.B.
 New attenuated myxoma recombinant virus and its use in the
 preparation of mixed vaccines against myxomatosis and rabbit
 hemorrhagic disease
 Patent: EP 0972840-A 1 19-JAN-2000;
 INST NAC INVEST TECN AGR ALIM (ES); FUNDACION PARA EL ESTUDIO Y DE
 (ES)

FEATURES
 source
 1. .78
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Early/late promoter"

BASE COUNT 30 a 13 c 9 g 26 t
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 Best Local Similarity 86.3%; Pred. No. 0.067;
 Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 5 AAAAATGAAATTTATTTTGGATATATAAGCGCGCCATGG 55
 DB 54 AAAAATGAAATTTATTTTGGATATATAAGCGCGATGG 4

RESULT 10
 AR105797/c
 LOCUS AR105797 6474 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 66 from patent US 6103244.
 ACCESSION AR105797
 VERSION AR105797.1 GI:12819862
 KEYWORDS
 SOURCE
 ORGANISM
 Unknown.
 Unknown.
 Unclassified.
 1 (bases 1 to 6474)
 Dorner, F., Scheiflinger, F., Falkner, F., Gunter, M. and Pfeleiderer, M.
 Methods for generating immune responses employing modified vaccinia
 of fowlpox viruses
 Patent: US 6103244-A 66 15-AUG-2000;
 Location/Qualifiers
 1. .6474

FEATURES
 source
 /organism="unknown"

BASE COUNT 1649 a 1533 c 1411 g 1881 t
 ORIGIN

Query Match 52.8%; Score 39.6; DB 6; Length 6474;
 Best Local Similarity 83.3%; Pred. No. 0.14;
 Matches 45; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 AAAAATGAAATTTATTTTGGATATATAAGCGCGCCATGGGCC 58
 DB 3964 AAAAATGAAATTTATTTTGGATATATAAGCGCCATGGGCC 3911

RESULT 11
 AX007102
 LOCUS AX007102 78 bp DNA linear PAT 06-SEP-2000
 DEFINITION Sequence 2 from Patent EP0972840.
 ACCESSION AX007102
 VERSION AX007102.1 GI:9994993
 KEYWORDS
 SOURCE
 ORGANISM
 synthetic construct.
 synthetic construct.

artificial sequences.
1 (bases 1 to 78)
AUTHORS Barcena,D.R., Parra,F.F., Blasco,L.R., Morales,C.M., Pages,M.A., Sanchez,V.J., Torres,T.J. and Vazquez,R.B.
TITLE New attenuated myxoma recombinant virus and its use in the preparation of mixed vaccines against myxomatosis and rabbit hemorrhagic disease
JOURNAL Patent: EP 0972840-A 2 19-JAN-2000;
INST NAC INVEST TECN AGR ALIM (ES); FUNDACION PARA EL ESTUDIO Y DE (ES)
FEATURES
source 1..78
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/db_xref="taxon:32630"
/note="Early/Late promoter"
BASE COUNT 26 a 9 c 13 g 30 t
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Best Local Similarity 86.0%; Pred. No. 0.13;
Matches 43; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 5 AAAAAATTGAATTTATTTTATTTTGGAAATATAAGCGCCGCATG 54
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Db 29 AAAAAATTGAATTTATTTTATTTTGGAAATATAAATTAATCTGACATG 78
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RESULT 12
LOCUS ARI05803 5532 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 72 from patent US 6103244.
ACCESSION ARI05803
VERSION ARI05803.1 GI:12819868
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5532)
AUTHORS Dörner,F., Schefflinger,F., Falkner,F.Günter. and Pfeleiderer,M.
TITLE Methods for generating immune responses employing modified vaccinia of fowlpox viruses
JOURNAL Patent: US 6103244-A 72 15-AUG-2000;
FEATURES
source 1..5532
/organism="unknown"
BASE COUNT 1482 a 1326 c 1263 g 1461 t
ORIGIN

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Best Local Similarity 79.3%; Pred. No. 0.24;
Matches 46; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 3 CCAAAATGAAATTTATTTTATTTTGGAAATATAAGCGCCGCATGCGCCG 60
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Db 3709 CTAATAATGAAATTTATTTTATTTTGGAAATATAAAGCGCTCATGAGCG 3652
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RESULT 13
LOCUS ARI05801 49 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 70 from patent US 6103244.
ACCESSION ARI05801
VERSION ARI05801.1 GI:12819866
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 49)
AUTHORS Dörner,F., Schefflinger,F., Falkner,F.Günter. and Pfeleiderer,M.
TITLE Methods for generating immune responses employing modified vaccinia of fowlpox viruses
JOURNAL Patent: US 6103244-A 70 15-AUG-2000;
FEATURES
Location/Qualifiers

source 1..49
/organism="unknown"
BASE COUNT 18 a 1 c 5 g 25 t
ORIGIN

Query Match 51.2%; Score 38.4; DB 6; Length 49;
Best Local Similarity 97.5%; Pred. No. 0.17;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCAAAATGAAATTTATTTTATTTTGGAAATATAA 42
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Db 9 CTAATAATGAAATTTATTTTATTTTGGAAATATAA 48
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RESULT 14
LOCUS AX326769 77 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 30 from Patent WO0172995.
ACCESSION AX326769
VERSION AX326769.1 GI:18097487
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Zauderer,M. and Smith,E.S.
TITLE Methods of producing a library and methods of selecting polynucleotides of interest
JOURNAL Patent: WO 0172995-A 30 04-OCT-2001;
UNIVERSITY OF ROCHESTER (US)
FEATURES
source 1..77
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Elovarv"
BASE COUNT 30 a 11 c 7 g 29 t
ORIGIN

Query Match 51.2%; Score 38.4; DB 6; Length 77;
Best Local Similarity 97.5%; Pred. No. 0.18;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AAAAAATGAAATTTATTTTATTTTGGAAATATAAGC 44
|||||
Db 77 AAAAAATGAAATTTATTTTATTTTGGAAATATAAGC 38
|||||

RESULT 15
LOCUS ARI05798 6811 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 67 from patent US 6103244.
ACCESSION ARI05798
VERSION ARI05798.1 GI:12819863
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 6811)
AUTHORS Dörner,F., Schefflinger,F., Falkner,F.Günter. and Pfeleiderer,M.
TITLE Methods for generating immune responses employing modified vaccinia of fowlpox viruses
JOURNAL Patent: US 6103244-A 67 15-AUG-2000;
FEATURES
source 1..6811
/organism="unknown"
BASE COUNT 1923 a 1567 c 1486 g 1835 t
ORIGIN

Query Match 51.2%; Score 38.4; DB 6; Length 6811;
Best Local Similarity 97.5%; Pred. No. 0.33;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCAAAATGAAATTTATTTTATTTTGGAAATATAA 42

DB 4988 CTAATAATTGAAATTTTATTTTGGAAATATAA 4949

Search completed: November 10, 2002, 06:52:46
Job time : 369.655 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:42:15 ; Search time 675 Seconds

(without alignments)
1799.499 Million cell updates/sec

Title: US-08-935-377-3

Perfect score: 1 GGCCTAAATGAAATTTTA.....GCCCGGCGCCCAACGGCGGA 75

Sequence: IDENTITY_NUC

Scoring table: Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST: *
1: em_estda: *
2: em_esthum: *
3: em_estln: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hlc: *
9: gb_est1: *
10: gb_est2: *
11: gb_hlc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_pln: *
21: em_gss_vit: *
22: em_gss_fun: *
23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rod: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	35.4	47.2	1201	17	CNS01651
2	33.4	44.5	158	10	AM297017 UI-H-BW0-
3	33.4	44.5	453	14	BM988219 UI-H-COO-
4	33	44.0	164	10	BE075111 PM1-BT058
5	32.2	42.9	1267	14	BO955325 AGENCOURT
6	31.8	42.4	586	14	BO578952 WHE2963_F

7	31.6	42.1	261	10	AM750324
c 8	31.6	42.1	962	12	BG177217
c 9	31.2	41.6	484	13	B1798613
c 10	31.2	41.6	501	10	AM515378
c 11	31	41.3	581	17	A2305110
c 12	31	41.3	602	17	A2989344
c 13	30.8	41.1	371	12	BF916182
c 14	30.6	40.8	1101	17	CNS00YWS
c 15	30.4	40.5	381	13	BM054767
c 16	30.4	40.5	909	17	AO743767 HS_-5501_A
c 17	30.2	40.3	573	13	BM382516
c 18	30.2	40.3	700	14	BO580344
c 19	30.2	40.3	797	17	BH155494
c 20	30	40.0	347	10	BE075085
c 21	30	40.0	607	9	A1570555
c 22	30	40.0	790	12	BG211548
c 23	30	40.0	872	17	AO752434 HS_-5566_B
c 24	30	40.0	1437	14	BO962773
c 25	29.8	39.7	431	10	AM947829
c 26	29.8	39.7	812	12	BE969600
c 27	29.8	39.7	1011	14	BM808393
c 28	29.8	39.7	1404	9	A1964281
c 29	29.6	39.5	470	13	B1349738
c 30	29.6	39.5	750	12	BF540838
c 31	29.6	39.5	829	13	BM393275
c 32	29.6	39.5	829	13	BM395278
c 33	29.6	39.5	932	10	AM730732 GA__Ea002
c 34	29.6	39.5	966	17	BH133169 ENTNE37TF
c 35	29.6	39.5	1035	14	BO735369 AGENCOURT
c 36	29.4	39.2	419	10	AM753884
c 37	29.4	39.2	468	10	AM297722
c 38	29.4	39.2	818	12	BE613522
c 39	29.4	39.2	1003	13	BM474859
c 40	29.2	38.9	230	9	AA339067
c 41	29.2	38.9	302	17	CNS03AZD
c 42	29.2	38.9	459	13	BM396122
c 43	29.2	38.9	617	10	AV645827
c 44	29.2	38.9	644	9	A1902252
c 45	29.2	38.9	1018	13	BM393128

ALIGNMENTS

RESULT 1
CNS01651 1201 bp DNA linear GSS 26-JUL-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC
DEFINITION BACN15M07 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION AL106303.1 GI:5621247
VERSION
KEYWORDS
SOURCE
ORGANISM

Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1201)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila genome project (EDGP) -
http://www.edgp.ebi.ac.uk/. This Drosophila melanogaster BAC
library (Dros-BAC) was made by Alain Billard at CERH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Boucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.
Location/Qualifiers

```

source
1. 1201
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACN15M07"
/clone_lib="DrosBAC"
/plasmid="pBelobAC11"
/note="end : 77"

BASE COUNT      286 a      290 c      192 g      283 t      150 others
ORIGIN

Query Match      47.2%; Score 35.4; DB 17; Length 1201;
Best Local Similarity 47.3%; Pred. No. 2e+02;
Matches 29; Conservative 22; Mismatches 10; Indels 0; Gaps 0;

OY 9 ATTGAATTTATTTTGTGAAATATAACGGCCGCAATGGCCGCCGCCGCCAA 68
    :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 960 RKKGTTTTTTTTTTTTTTKKKDWTTTAACTGCTKTSCKMGSGHCCSCSCCM 901
OY 69 C 69
    :
DB 900 M 900

RESULT 2
AM297017      158 bp      mRNA      linear      EST 16-JAN-2000
LOCUS
DEFINITION   UI-H-BM0-aJf-d-09-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone
IMAGE:2731457 3', mRNA sequence.
ACCESSION   AM297017
VERSION     AM297017.1 GI:6703653
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 158)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapsb-remail.nih.gov
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. cDNA library Preparation: M.B. Soares Lab Clone distribution:
            NCI-CGAP clone distribution information can be found through the
            I.M.A.G.E. Consortium/ILNI at:
            www-bio.lnl.gov/bdrp/image/image.html The following repetitive
            elements were found in this cDNA sequence: 99-142,
            >GC_rich#low_complexity
            Seq primer: M13 Forward
            POLYA=yes.

FEATURES
SOURCE
Location/Qualifiers
1..158
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2731457"
/clone_lib="NCI CGAP Sub6"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; NCI_CGAP_Sub6
is a subtracted library derived from BM, which consists of
a mixture of four normalized libraries: NCI CGAP Brn50,
NCI CGAP Lu13, NCI CGAP Ov18, GBC1. The NCI_CGAP_Sub6
library had 7 million recombinants. A single-stranded DNA
preparation of BM was used as a tracer in a subtractive
hybridization with a driver comprising the IMAGE pool
(NCI_CGAP_Kid3 pool 1 ILAM 3334-3337, 3682-3683,
3798-3803 (IMAGE Clonoids 1322376-1323911,
1456008-1456775, 1500552-1502855); NCI_CGAP_Kid5 pool 1
ILAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clonoids
1323912-1325831, 1471368-1472903, 1492104-1493255));

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BASE COUNT      17 a      62 c      43 g      36 t
ORIGIN

Query Match      44.5%; Score 33.4; DB 10; Length 158;
Best Local Similarity 72.9%; Pred. No. 1.9e+03;
Matches 43; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 16 TTTTATTTTGTGAAATATAAGCGCCGCAATGGCCGCCGCCCAACGCGG 74
    |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
DB 1 TTTTATTTTGTGTAAGACGCGCTTTAATGAGGCCGCCGCCGCCGCCGCCG 59

RESULT 3
BM988219      453 bp      mRNA      linear      EST 17-JUN-2002
LOCUS
DEFINITION   UI-H-CO0-atn-g-02-0-UI.s1 NCI_CGAP_Sub9 Homo sapiens cDNA clone
IMAGE:5861931 3', mRNA sequence.
ACCESSION   BM988219
VERSION     BM988219.1 GI:19707608
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 453)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapsb-remail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
            cDNA library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Clone distribution information can be found
            through the I.M.A.G.E. Consortium/ILNI at: http://image.lnl.gov
            The following repetitive elements were found in this cDNA
            sequence: 100-143, >GC_rich#low_complexity 347-410,
            >GC_rich#low_complexity
            Seq primer: M13 FORWARD
            POLYA=yes.

FEATURES
SOURCE
Location/Qualifiers
1..453
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5861931"
/clone_lib="NCI CGAP Sub9"
/tissue_type="mixed"
/dev_stage="mixed"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73-Pac (Pharmacia) with a modified

```

FEATURES	source
LOCUS	BE075111
DEFINITION	PM1-BT0585-110200-003-h11 BT0585 Homo sapiens cDNA, mRNA sequence.
ACCESSION	BE075111
VERSION	BE075111.1 GI:8423655
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 164) Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsumura, A., Bala, G. S., Simpson, D. H., Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
COMMENT	20202663 Contact: Simpson A.J.G. Laboratory of Cancer Genetics Rui Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=6t2-PM1-BT0585-110200-003-h11&t3=2000-02-11&t4=1) Seq primer: puc 18 forward High quality sequence stop: 127. Location/Qualifiers 1..164 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_id="BT0585"

QY	1	GGCCCAAAATTAATTTATTTTGGATATATAAGCGCGCCATGGGCGG 60	42.9%	Score 32.2;	DB 14;	Length 1267;	
Db	807	GGCCCAAAATTAAGAGCTTTTATTTTAAATAAAAGTCCGCGCCCAAGGGCCAG 748	70.5%	Pred. No. 8.3e+02;			
QY	61	G 61	0;	Mismatches 18;	Indels 0;	Gaps 0;	
QY	1						

Db 747 G 747

RESULT 6
LOCUS B0578952 586 bp mRNA linear EST 19-JUN-2002
DEFINITION B0578952.F04.K07ZS wheat dormant embryo cDNA library Triticum aestivum cDNA clone WHE2963_F04_K07, mRNA sequence.
ACCESSION B0578952
VERSION B0578952.1 GI:21482269
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticaceae; Triticum.
1 (bases 1 to 586)
REFERENCE Anderson,O.D., Chao,S., Chin,A., Close,T.J., Doherty,L., Fenton,R.D., Iazo,G.R., Kausch,C.J., Walker-Simmons,M.K. and Wilson,C. The structure and function of the expressed portion of the wheat genomes - Dormant embryo cDNA library
JOURNAL Unpublished (2001)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: SK primer.
Location/Qualifiers
1..586
/organism="Triticum aestivum"
/cultivar="Brevor"
/db_xref="taxon:4565"
/clone_lib="WHE2963_F04_K07"
/clone_lib="Wheat dormant embryo cDNA library"
/tissue_type="Seed embryo"
/dev_stage="Mature seed"
/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Plants were grown to seed maturity under conditions favoring seed dormancy (L. Doherty at K. Walker-Simmons lab, Washington State University, Pullman, WA). Embryos were cut from mature dormant seed (Doherty). Total RNA was prepared from these embryos, polyA was purified, a cDNA library was made, and the cDNA clones were in vivo excised to give phagescript phagmids in the T7 Close lab at the University of California, Riverside (Chin, Fenton). Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 145 a 143 c 141 g 157 t
ORIGIN

Query Match 42.4%; Score 31.8; DB 14; Length 586;
Best Local Similarity 71.2%; Pred. No. 1.7e+03;
Matches 42; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

OY 16 TTTTATTTTTTTTGGAAATATAAGCGCGCCCATGGCGCGCGCCCAACGGCGG 74
|||||
Db 4 TTTTATTTTTTTTGGAAACAGAGAGCGACGCAATGACGCGCGCGCGG 62

RESULT 7
LOCUS AW750324 261 bp mRNA linear EST 28-APR-2000
DEFINITION AW750324.PM1-BT0585-310100-002-d03 BT0585 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW750324
VERSION AW750324.1 GI:7665256
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 261)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.O.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the RAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1&t2=PM1-BT0585-310100-002-d03&t3=2000-01-31&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 143.
Location/Qualifiers
1..261
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT0585"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue RNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 74 a 46 c 57 g 84 t
ORIGIN

Query Match 42.1%; Score 31.6; DB 10; Length 261;
Best Local Similarity 65.7%; Pred. No. 3.1e+03;
Matches 46; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

OY 5 AAAAATTGAATTTTATTTTGGAAATATPAAGCGCGCCATGGCGCGCGG 64
|||||
Db 118 AAGAGAGAAATTTTATTTTGGAAATGAAATGCGCCCATATAGGGTTT 177

OY 65 CCAACGCGG 74
|||||
Db 178 TTTAAGGAG 187

RESULT 8
LOCUS BG177217/c 962 bp mRNA linear EST 06-FEB-2001
DEFINITION BG177217 602314394F1 NIH-MGC_85 Homo sapiens cDNA clone IMAGE:4420366 5', mRNA sequence.
ACCESSION BG177217
VERSION BG177217.1 GI:12683920
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 962)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL , Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Louis Staudt, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
Plate: LLM10157 row: k column: 23
High quality sequence stop: 403.

FEATURES
source Location/Qualifiers
 ..962
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4420366"
 /clone_1lb="NIH_MGC_85"
 /tissue_type="lymphoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: lymph; Vector: pCMV-Sport6; site_1: NotI; site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC library."

BASE COUNT 278 a 227 c 231 g 225 t 1 others

ORIGIN

Query Match 42.1%; Score 31.6; DB 12; Length 962;
Best Local Similarity 65.7%; Pred. NO. 1.3e+03;

Matches	46;	Conservative	0;	Mismatches	24;	Indels	0;	Gaps	0;
Oy	5	AAAAATTGAATTTATTTTTTTTTTTTGAAATAAAGCGGCGCCCATGGCGGCCGCGG	64						
Db	397	AGAAATGGAATTTTTTTTTTTTTTTTTTAAAAGGTCTGCCGCCGACATGG	338						
Oy	65	CCAACGGCGG	74						
Db	337	CTCAGCCTG	328						

RESULT 9
BI798613/c

LOCUS BI798613 484 bp mRNA linear EST 02-OCT-2001

DEFINITION H112D05 Endosperm library from Oryza sativa (10 days after anthesis).

ACCESSION BI798613

VERSION BI798613.1 GI:15850337

KEYWORDS EST.

SOURCE Oryza sativa.

ORGANISM Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartioideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 484)
Dong,H.T., Li,D.B., Zhang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu
R.H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.
A Gene Expression Screen in Oryza sativa
Unpublished (2001)

TITLE Laboratory of Functional Genetics
JOURNAL Bio-technology Institute of Zhejiang University
COMMENT Kaituan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
Fax: 0086-571-86961525
Email: htdong@zjuem.zju.edu.cn
Seq primer: M13 forward primer.
Location/Qualifiers
 ..484
 /organism="Oryza sativa"
 /db_xref="taxon:4530"
 /clone="H112D05"
 /clone_1lb="Endosperm library from Oryza sativa (10 days

FEATURES
source

Query Match	Best Local Similarity	Matches	41.6%;	Score 31.2;	DB 13;	Length 484;	
Query Match	Best Local Similarity	Matches	41.6%;	Score 31.2;	DB 13;	Length 484;	
Best Local Similarity	70.0%;	Pred. No. 2.5e+03;					
Matches	42;	Conservative	0;	Mismatches	18;	Indels	0;
Gap	0;						
DB	480	TTTTTTT	TTTTTTT	TTTTTTT	TTTTTTT	TTTTTTT	TTTTTTT
LOCUS	AM515378	501 bp	MRNA	linear	EST 03-MAR-2000		
DEFINITION	XU96G01.x1 NCI_CGAP	UT2 Homo sapiens	cDNA clone IMAGE:2809536	3			
ACCESSION	AM515378						
VERSION	AM515378.1	GI:7153460					
KEYWORDS	EST.						
SOURCE	human.						
ORGANISM	Homo sapiens						
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.						
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.						
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),						
COMMENT	Tumor Gene Index						
	Unpublished (1997)						
	Contact: Robert Strausberg, Ph.D.						
	Email: cgapbs-rt@mail.nih.gov						
	Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.						
	Emmert-Buck, M.D., Ph.D.						
	cDNA library Preparation: Life Technologies, Inc.						
	DNA library Arrayed by: Greg Lennon, Ph.D.						
	DNA Sequencing by: Washington University Genome Sequencing Center						
	Clone distribution: NCI-CGAP clone distribution information can be						
	found through the I.M.A.G.E. Consortium/LLNL at:						
	Image.llnl.gov/image/html/iresources.shtml						
	Seq primer: -40UP from Glbco						
	High quality sequence stop: 415.						
FEATURES	Location/Qualifiers						
source	1.501						
	/organism="Homo sapiens"						
	/db_xref="taxon:9606"						
	/clone="IMAGE:2809536"						
	/clone_1lb="NCI_CGAP UT2"						
	/tissue_type="moderately-differentiated endometrial						
	adenocarcinoma, 3 pooled tumors"						
	/lab_host="DH10B"						
	/note="Organ: uterus; Vector: pCMV-Sport6; Site: 1; Salt;						
	Site: 2; NCI; Cloned unidirectionally. Primer: Oligo dT.						
	Average insert size 1.85 kb. Life Technologies catalog #:						
	11539-012"						
BASE COUNT	126 a	68 c	136 g	170 t	1	others	
ORIGIN							
Query Match	Best Local Similarity	Matches	41.6%;	Score 31.2;	DB 10;	Length 501;	
Best Local Similarity	70.0%;	Pred. No. 2.4e+03;					
Matches	42;	Conservative	0;	Mismatches	18;	Indels	
Gap	0;						
DB	10	TTGAAATTTTATTTT	TTTTTTT	TTGGAATATATAAGCGCGCCCATGGCGCCGCGCCCAAC	69		
	111	1111	11111111111	111	111	111	
	4	TTGTTTTTTTTTTTT	TTTTTTT	TTGCAAAAAAATGAGCGCCATGGCGGCTTGCTGAAC	63		
RESULT 11							
2305110/c							

LOCUS	AZ305110	581 bp	DNA	linear	GSS-29-SEP-2000
DEFINITION	IM0005P05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0005P05 R, DNA sequence.				
ACCESSION	AZ305110				
VERSION	AZ305110.1	GI:10341800			
KEYWORDS	GSS.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 581)				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert length: 10000 Std Error: 0.00 Plate: 0005 row: P column: 05 Seq primer: CACACAGAAACACCTATGACC Class: plasmid ends High quality sequence stop: 581. Location/Qualifiers 1..581 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC1M0005P05" /clone_id="Mouse 10kb plasmid UUGC1M library" /sex="male" /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi14732114 gb AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."				
BASE COUNT	169 a	139 c	153 g	120 t	
ORIGIN					
Query Match	41.3%	Score 31:	DB 17:	Length 581:	
Best Local Similarity	78.7%;	Pred. No. 2.4e+03;			
Matches 377	Conservative 0;	Mismatches 10;	Indels 0;	Gaps 0;	
Oy	10 TTGAATTTTATTTTTTTTTTTTGGAATATTAAAGCGGCCCATGGG 56				
Db	341 TTGAATTTTTTTTTTTCTTTTGTGAAAATCCAGTGGCGCTTAAGG 295				
RESULT 12					
12989344					

LOCUS	602 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	2M0272208R Mouse 10kb plasmid U06C2M library Mus musculus genomic			
ACCESSION	Z4289344			
VERSION	Z4289344.1			
KEYWORDS	GI:13860571			
SOURCE	GSS.			
ORGANISM	house mouse.			
REFERENCE	Mus musculus			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.			
	1 (bases 1 to 602)			
	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duvall,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,J., Rose,M., Rogase,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D., Weiss,R.			
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0272 row: J column: 08 Seq primer: CACACAGGAACACGTATGACC Class: plasmid ends High quality sequence stop: 602.			
FEATURES	Location/Qualifiers			
SOURCE	1..602			
	/organism="Mus musculus"			
	/strain="C57BL/6J"			
	/db_xref="taxon:10090"			
	/clone="U06C2M0272J08"			
	/clone_1ib="Mouse 10kb plasmid U06C2M library"			
	/sex="Female"			
	/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"			
	/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g11473211419b/AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."			
BASE COUNT	136 a	147 c	121 g	198 t
ORIGIN				
Query Match	41.3%	Score 31;	DB 17;	Length 602;
Best Local Similarity	78.7%;	Pred. No. 2.3e+03;		
Matches	37; Conservative	0; Mismatches	10;	Indels 0; Gaps 0;
QY	10	TTGAATTTTAAATTTTTTTTGGAAATATTAAGCGCGCCAGCATGG	56	
DB	120	TTGAATTTTATTTTCTTTTGGAAATATCAATCGCGCCGCTAAAGG	166	
RESULT 13				
BF916182				

LOCUS BF916182 371 bp mRNA linear EST 18-JAN-2001
 DEFINITION RCL-UT0083-091200-023-b06 UT0083 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF916182
 VERSION BF916182.1 GI:12307640
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 371)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,M.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
 Brunsehl,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 'M.J.', Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 JOURNAL MEDLINE 2002663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-UT0083-
 091200-023-b06&t3=2000-12-09&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 17
 High quality sequence stop: 310.
 Location/Qualifiers
 1..371
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="UT0083"
 /dev_stage="Adult"
 /note="Organ: uterus_tumor; Vector: puc18; Site:1; SmaI;
 Site:2; SmaI: A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No.196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 BASE COUNT 76 a 102 c 80 g 113 t
 ORIGIN
 Query Match 41.1%; Score 30.8; DB 12; Length 371;
 Best Local Similarity 63.5%; Pred. No. 3.5e+03;
 Matches 47; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
 QY 1 GGCAGAAATGGAATTTATTTTGTGGAATATAAGCGCGCCATGCGCCG 60
 Db 275 GGCCTCTATTTTATTTTGTGGAAGAAAGAACCCCGCGGCGCA 334
 QY 61 GCCGCCAAGCGCG 74
 Db 335 GCGGGAGAGCGAGC 348

RESULT 14
 CNS00YWS 1101 bp DNA linear GSS 26-JUL-1999
 LOCUS DEFINITION Drosophila melanogaster genome survey sequence 17 end of BAC
 BACN01A18 of DrosBAC library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION AL096911
 VERSION AL096911.1 GI:5608522
 KEYWORDS GSS.

SOURCE Drosophila melanogaster.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peerygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 1101)
 Genoscope.
 Direct Submision
 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the European Drosophila Genome Project (EDGP) -
 http://www.edgp.edl.ac.uk -. This Drosophila melanogaster BAC
 library (Dros BAC) was made by Alain Billard at CEPH (Centre
 d'Etude du Polymorphisme Humain) with funding provided by a MRC
 project grant. The DNA was prepared from embryos by Alain Bucheton
 and Genevieve Payan. It has been constructed in the vector
 pBelBAC11.
 FEATURES Location/Qualifiers
 1..1101
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 /db_xref="taxon:7227"
 /clone_lib="BACN01A18"
 /clone_lib="DrosBAC"
 /plasmid="pBelBAC11"
 /note="end : 17"
 BASE COUNT 270 a 179 c 175 g 330 t 147 others
 ORIGIN
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 Best Local Similarity 49.2%; Pred. No. 1.9e+03;
 Matches 32; Conservative 17; Mismatches 16; Indels 0; Gaps 0;
 QY 2 GCCAGAAATGGAATTTTATTTTGTGGAATATAAGCGCGCCATGCGCCG 61
 Db 1000 SCCAAMAATTWAMAMTTTTTTTTTTTGTGAGDGVVSVACCCCGCGRCCG 941
 QY 62 CCGCC 66
 Db 940 TTGMC 936

RESULT 15
 BM054767 381 bp mRNA linear EST 12-MAR-2002
 LOCUS DEFINITION le84h05.x1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
 cDNA clone IMAGE:5673825 3', mRNA sequence.
 ACCESSION BM054767
 VERSION BM054767.1 GI:16812115
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 381)
 Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
 Lemshika,I., Scaer,J., Brestelli,J., Gradwohl,G., Clifton,S.,
 Hillier,L., Marra,M., Page,D., Wylie,T., Martin,J., Blistain,A.,
 Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
 M., Gibbons,M., McCann,R., Cole,R., Tsagarisvill,R., Williams,T.,
 Jackson,Y. and Bowers,Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Douglas Melton DNA sequencing by:

[illegible]

XX	PA	(UYRP) UNIV ROCHESTER.
XX	PI	Zauderer M, Smith ES;
XX	DR	WPI; 2001-570897/64.
XX	PT	Selecting target polynucleotides, particularly toxic genes, involves
XX	PT	introducing a library of insert polynucleotides into a host cell
XX	PT	population, where the target polynucleotide promotes cell death -
XX	PS	Disclosure: Fig 1; 359pp; English.
XX	CC	The present invention relates to a method for selecting a target
XX	CC	polynucleotide. The method comprises introducing into a host cell
XX	CC	population a library of insert polynucleotides, where expression of the
XX	CC	target polynucleotide directly or indirectly promotes host cell death.
XX	CC	The cells are cultured and the insert polynucleotides are collected from
XX	CC	the cells which die. The method is useful for selecting target
XX	CC	polynucleotides, particularly polynucleotides which alter cell phenotypes
XX	CC	of induce or inhibit cell death. The method can be used to isolate toxic
XX	CC	genes such as tumour suppressors. The present sequence was used to
XX	CC	illustrate the method of the the present invention.
XX	SQ	Sequence 75 BP; 19 A; 16 C; 19 G; 21 T; 0 other;
XX	Query Match	100.0%; Score 75; DB 22; Length 75;
XX	Best Local Similarity	100.0%; Pred. No. 1,5e-12;
XX	Matches 75; Conservative	0; Mismatches 0; Indels 0; Gaps 0
XX	OY	1 GGGCAAAATTTGAAATTTATTTTTTTTTTTGGAAATATAAAGCGCGCCCATGGCCCG 60
XX		
XX	Db	1 GGGCAAAATTTGAAATTTATTTTTTTTTTTGGAAATATAAAGCGCGCCCATGGCCCG 60
XX	OY	61 GCGCGCAAGCGCGGA 75
XX		
XX	Db	61 GCGCGCAAGCGCGGA 75
XX	RESULT 3	
XX	AAD31776	
XX	ID	AAD31776 standard; DNA; 75 BP.
XX	XX	AAD31776;
XX	DT	18-JUN-2002 (first entry)
XX	DE	pE/Ltk vector comprising E/L promoter and vaccinia virus tk DNA.
XX	KW	Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;
XX	KW	vaccine; Immune response; cytostatic; pE/Ltk vector; thymidine kinase;
XX	OS	ds.
XX	OS	Vaccinia virus.
XX	SS	Synthetic.
XX	Key	Location/Qualifiers
XX	FT	52..75
XX	FT	/tag= a
XX	FT	/product= "Thymidine kinase protein"
XX	PN	US2002018785-A1.
XX	PD	14-FEB-2002.
XX	PF	02-APR-2001; 2001US-0822250.
XX	PR	22-SEP-1997; 97US-0935377.
XX	PA	(UYRP) UNIV ROCHESTER.
XX	PI	Zauderer M;

Query Match	Best Local Similarity	Score	DB	Length
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	100.0%;	75;	24;	75;
QY 1 GGGCAAAATTAATTTATTTTGGATTAAGCGCGCCATGGGCGG 60				
Db 1 GGGCAAAATTAATTTATTTTGGATTAAGCGCGCCATGGGCGG 60				
QY 61 GCCGCCAACGGCGGA 75				
Db 61 GCCGCCAACGGCGGA 75				

RESULT 4
ABA01484
ABA01484 standard; DNA: 59 BP.

QY	Db
1 GGGCAAAATTAATTTATTTTGGATTAAGCGCGCCATGGGCGG 60	1 GGGCAAAATTAATTTATTTTGGATTAAGCGCGCCATGGGCGG 60
61 GCCGCCAACGGCGGA 75	61 GCCGCCAACGGCGGA 75

04-FEB-2002 (first entry)
PCR primer MM438.
PCR primer: cell death; toxic gene; tumour suppressor; ss.
Synthetic.
WO200172995-A2.
04-OCT-2001.
28-MAR-2001; 2001WO-US09953.
28-MAR-2000; 2000US-0192586.
10-MAY-2000; 2000US-0203343.
23-JAN-2001; 2001US-0263226.
27-FEB-2001; 2001US-0271426.

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PA      (UYRP ) UNIV ROCHESTER.
XX
XX
PI      Zauderer M, Smith ES;
DR
XX      WPI: 2001-570897/64 .
XX
XX      Selecting target polynucleotides, particularly toxic genes, involves
PT      introducing a library of insert polynucleotides into a host cell
PP      population, where the target polynucleotide promotes cell death -
XX
XX      Example 1; Page 135; 359pp; English.
XX
CC      The present invention relates to a method for selecting a target
CC      polynucleotide. The method comprises introducing into a host cell
CC      population a library of insert polynucleotides, where expression of
CC      target polynucleotide directly or indirectly promotes host cell death
CC      The cells are cultured and the insert polynucleotides are collected
CC      the cells which die. The method is useful for selecting target
CC      polynucleotides, particularly polynucleotides which alter cell phenom
CC      of induce or inhibit cell death. The method can be used to isolate t
CC      genes such as tumour suppressors. The present sequence is a PCR prim
CC      which was used in an example from the present invention.
XX
SQ      Sequence 59 BP; 16 A; 10 C; 12 G; 21 T; 0 other;
XX
XX      Query Match          78.7%; Score 59; DB 22; Length 59;
XX      Best Local Similarity 100.0%; Pred. No. 5.6e+08;
XX      Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps
OY      1 GCCCAAAATTTGAATTTTATTTTTTTTGGCAATTAAAGCGGCCCATGGGCC 59
Db       1 GGCCAAAATTTGAATTTTATTTTTTTTTTTTGGCAATTAAAGCGGCCCATGGGCC 59
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
RESULT 5
ABA01485/C
ID      ABA01485 standard; DNA; 59 BP.
XX
XX      ABA01485;
AC      XX
XX      04-FEB-2002 (first entry)
DT      XX
DE      PCR primer MM439.
XX
XX      PCR primer; cell death; toxic gene; tumour suppressor; ss.
KW      XX
OS      Synthetic.
PN      WO200172995-A2.
XX
XX      04-OCT-2001.
PD      XX
PE      28-MAR-2001; 2001WO-US099953.
XX
XX      28-MAR-2001; 2000US-0192586.
PR      10-MAY-2000; 2000US-0203343.
PR      23-JAN-2001; 2001US-0263226.
PR      27-FEB-2001; 2001US-0271426.
XX
XX      (UYRP ) UNIV ROCHESTER.
PA
PI      Zauderer M, Smith ES;
XX
XX      WPI: 2001-570897/64 .
DR
XX      Selecting target polynucleotides, particularly toxic genes, involves
PT      introducing a library of insert polynucleotides into a host cell
PP      population, where the target polynucleotide promotes cell death -
XX
XX      Example 1; Page 135; 359pp; English.
XX
CC      The present invention relates to a method for selecting a target
CC      polynucleotide. The method comprises introducing into a host cell

```

CC population a library of insert polynucleotides, where expression of the
CC target polynucleotide directly or indirectly promotes host cell death.
CC The cells are cultured and the insert polynucleotides are collected from
CC the cells which die. The method is useful for selecting target
CC polynucleotides, particularly polynucleotides which alter cell phenotypes
CC of induce or inhibit cell death. The method can be used to isolate toxic
CC genes such as tumour suppressors. The present sequence is a PCR primer,
CC which was used in an example from the present invention.
XX
SQ Sequence 59 BP; 21 A; 12 C; 10 G; 16 T; 0 other;
Query Match 78.7%; Score 59; DB 22; Length 59;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 AAAAAATTGAATTTATTTTGTGGAATATATAAGCGCGCCCATGGCCGCC 63
DB 59 AAAAAATTGAATTTATTTTGTGGAATATATAAGCGCGCCCATGGCCGCC 1
RESULT 6
AAD31796
ID AAD31796 standard; DNA; 59 BP.
XX
AC AAD31796;
XX
DT 18-JUN-2002 (first entry)
XX
DE MM438 oligonucleotide used to construct pE/Ltk plasmid.
XX
KW Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;
KW vaccine; immune response; cytostatic; pE/Ltk plasmid; thymidine kinase;
KW ds.
XX
OS Unidentified.
XX
PN US2002018785-A1.
XX
PD 14-FEB-2002.
XX
PF 02-APR-2001; 2001US-0822250.
XX
PR 22-SEP-1997; 97US-0935377.
XX
PA (UYRP) UNIV ROCHESTER.
PI Zauderer M;
XX
DR WPI; 2002-239252/29.
XX
PT Representational Difference Analysis method for identification of
PT antigens recognized by cytotoxic T cells and specific for human tumours,
PT comprises improved selection of genes encoding target antigens -
XX
PS Example 9; Page 23; 54pp; English.
XX
CC The present invention relates to novel methods for the identification
CC of antigens recognised by cytotoxic T cells (CTLs) and specific for
CC human tumours, cancers and infected cells. The method involves screening
CC the products of an expression library generated from DNA/RNA of a cell
CC expressing a target epitope with cytotoxic T cells generated against
CC the cell to identify DNA clones expressing target epitope or providing
CC cytotoxic T cells specific for a gene product differentially expressed
CC by a cell and measuring the cross-reactivity of the cytotoxic T cells
CC for cells expressing a target epitope in which the target epitope is
CC identified as a gene product inducing cytotoxic T cells. The method is
CC useful for identifying a target epitope or antigen specific for a tumour
CC cell. The target epitope is also useful for identifying target antigens
CC in other target cells against which it is desirable to induce cell-
CC mediated immunity. The antigen identified by the method is useful
CC in immunogenic compositions and vaccine preparations to induce the
CC regression of tumours, cancers and infections in mammals. The invention
CC also relates to vaccinia viral vectors which are useful for treating

CC tumour-bearing mammals, including humans to generate immune response
CC against the tumour cells. They are also useful for immunising or
CC vaccinating tumour-free subjects to prevent tumour formation. The
CC present DNA sequence is an oligonucleotide which is used to construct
CC pE/Ltk (thymidine kinase) plasmid comprising a synthetic early/late
CC (E/L) promoter and vaccinia virus tk DNA fragment. This oligo is used
CC in the exemplification of the invention.
XX
SQ Sequence 59 BP; 16 A; 10 C; 12 G; 21 T; 0 other;
Query Match 78.7%; Score 59; DB 24; Length 59;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GCGCAAAATTTGAATTTATTTTGTGGAATATATAAGCGCGCCCATGGCC 59
DB 1 GCGCAAAATTTGAATTTATTTTGTGGAATATATAAGCGCGCCCATGGCC 59
RESULT 7
AAD31797/C
ID AAD31797 standard; DNA; 59 BP.
XX
AC AAD31797;
XX
DT 18-JUN-2002 (first entry)
XX
DE MM439 oligonucleotide used to construct pE/Ltk plasmid.
XX
KW Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;
KW vaccine; immune response; cytostatic; pE/Ltk plasmid; thymidine kinase;
KW ds.
XX
OS Unidentified.
XX
PN US2002018785-A1.
XX
PD 14-FEB-2002.
XX
PF 02-APR-2001; 2001US-0822250.
XX
PR 22-SEP-1997; 97US-0935377.
XX
PA (UYRP) UNIV ROCHESTER.
PI Zauderer M;
XX
DR WPI; 2002-239252/29.
XX
PT Representational Difference Analysis method for identification of
PT antigens recognized by cytotoxic T cells and specific for human tumours,
PT comprises improved selection of genes encoding target antigens -
XX
PS Example 9; Page 23; 54pp; English.
XX
CC The present invention relates to novel methods for the identification
CC of antigens recognised by cytotoxic T cells (CTLs) and specific for
CC human tumours, cancers and infected cells. The method involves screening
CC the products of an expression library generated from DNA/RNA of a cell
CC expressing a target epitope with cytotoxic T cells generated against
CC the cell to identify DNA clones expressing target epitope or providing
CC cytotoxic T cells specific for a gene product differentially expressed
CC by a cell and measuring the cross-reactivity of the cytotoxic T cells
CC for cells expressing a target epitope in which the target epitope is
CC identified as a gene product inducing cytotoxic T cells. The method is
CC useful for identifying a target epitope or antigen specific for a tumour
CC cell. The target epitope is also useful for identifying target antigens
CC in other target cells against which it is desirable to induce cell-
CC mediated immunity. The antigen identified by the method is useful
CC in immunogenic compositions and vaccine preparations to induce the
CC regression of tumours, cancers and infections in mammals. The invention
CC also relates to vaccinia viral vectors which are useful for treating
CC tumour-bearing mammals, including humans to generate immune response

CC against the tumour cells. They are also useful for immunising or
CC vaccinating tumour-free subjects to prevent tumour formation. The
CC present DNA sequence is an oligonucleotide which is used to construct
CC pE/Ltk (thymidine kinase) plasmid comprising a synthetic early/late
CC (E/L) promoter and vaccinia virus tk DNA fragment. This oligo is used
CC in the exemplification of the invention.

XX Sequence 59 BP; 21 A; 12 C; 10 G; 16 T; 0 other;

Query Match 78.7%; Score 59; DB 24; Length 59;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 AAAAAATGAAATTTATTTTATTTTGGAAATATAAGCGCGCCATGCGCCGCC 63
DB 59 AAAAAATGAAATTTATTTTATTTTGGAAATATAAGCGCGCCATGCGCCGCC 1

RESULT 8
ABA01491
ID ABA01491 standard; DNA; 77 BP.

XX ABA01491;

XX 04-FEB-2002 (first entry)

DE PCR primer E10va.

XX PCR primer; cell death; toxic gene; tumour suppressor; ss.

XX Synthetic.

XX WO200172995-A2.

XX 04-OCT-2001.

XX 28-MAR-2001; 2001WO-US09953.

XX 28-MAR-2000; 2000US-0192586.

XX 10-MAY-2000; 2000US-020343.

XX 23-JAN-2001; 2001US-0263226.

XX 27-FEB-2001; 2001US-02711426.

XX (UYRP) UNIV ROCHESTER.

XX Zauderer M, Smith ES;

XX WPI; 2001-570897/64.

XX Example 1; Page 136; 359pp; English.

XX The present invention relates to a method for selecting a target
XX polynucleotide. The method comprises introducing into a host cell
XX a population a library of insert polynucleotides, where expression of the
XX target polynucleotide directly or indirectly promotes host cell death.
XX The cells are cultured and the insert polynucleotides are collected from
XX the cells which die. The method is useful for selecting target
XX polynucleotides, particularly polynucleotides which alter cell phenotypes
XX of induce or inhibit cell death. The method can be used to isolate toxic
XX genes such as tumour suppressors. The present sequence is a PCR primer,
XX which was used in an example from the present invention.

XX Sequence 77 BP; 29 A; 7 C; 11 G; 30 T; 0 other;

Query Match 56.5%; Score 42.4; DB 22; Length 77;
Best Local Similarity 97.7%; Pred. No. 0.0033;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGCCAAAAATGAAATTTATTTTATTTTGGAAATATAAGC 44

DB 1 GGCCAAAAATGAAATTTATTTTATTTTGGAAATATAAGC 44

RESULT 9
AAD31803
ID AAD31803 standard; DNA; 77 BP.

XX AAD31803;

XX 18-JUN-2002 (first entry)

DE E10va oligonucleotide used to construct pE/Ltk-ova plasmid.

XX Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;

XX Immune response; cytostatic; pE/Ltk-ova plasmid; thymidine kinase;

XX vaccine; ovalbumin; ds.

XX Unidentified.

XX US2002018785-A1.

XX 14-FEB-2002.

XX 02-APR-2001; 2001US-0822250.

XX 22-SEP-1997; 97US-0935377.

XX (UYRP) UNIV ROCHESTER.

XX Zauderer M;

XX WPI; 2002-239252/29.

XX Example 9; Page 23; 54pp; English.

XX The present invention relates to novel methods for the identification
XX of antigens recognised by cytotoxic T cells (CTLs) and specific for
XX human tumours, cancers and infected cells. The method involves screening
XX the products of an expression library generated from DNA/RNA of a cell
XX expressing a target epitope with cytotoxic T cells generated against
XX the cell to identify DNA clones expressing target epitope or providing
XX cytotoxic T cells specific for a gene product differentially expressed
XX by a cell and measuring the cross-reactivity of the cytotoxic T cells
XX for cells expressing a target epitope in which the target epitope is
XX identified as a gene product inducing cytotoxic T cells. The method is
XX useful for identifying a target epitope or antigen specific for a tumour
XX cell. The target epitope is also useful for identifying target antigens
XX in other target cells against which it is desirable to induce cell-
XX mediated immunity. The antigen identified by the method is useful
XX in immunogenic compositions and vaccine preparations to induce the
XX regression of tumours, cancers and infections in mammals. The invention
XX also relates to vaccinia viral vectors which are useful for treating
XX tumour-bearing mammals, including humans to generate immune response
XX against the tumour cells. They are also useful for immunising or
XX vaccinating tumour-free subjects to prevent tumour formation. The
XX present DNA sequence is an oligonucleotide which is used to construct
XX pE/Ltk (thymidine kinase)-ova plasmid comprising a synthetic E/L
XX (early/late) promoter, tk DNA fragment and a DNA encoding cytotoxic
XX T-cell epitope for ovalbumin. This oligo is used in the exemplification
XX of the invention.

XX Sequence 77 BP; 29 A; 7 C; 11 G; 30 T; 0 other;

Query Match 56.5%; Score 42.4; DB 24; Length 77;
Best Local Similarity 97.7%; Pred. No. 0.0033;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGCCAAAAATGAAATTTATTTTATTTTGGAAATATAAGC 44

```
Db      1  GGGCAAAATGCAATTTATTTTGGAAATATAACC 44
|||||
RESULT 10
ID      AAT78340 standard; DNA; 84 BP.
XX
AC      AAT78340;
XX
DE      13-OCT-1997 (first entry)
XX
DE      Chimeric virus construction oligonucleotide oselp1.
XX
KM      Recombinant eukaryotic cytoplasmic DNA virus; vaccine production;
KM      double selection marker; attenuated live pox virus; HIV; HBV;
KM      surface antigen gene; encephalitis; tick-borne; ss.
XX
OS      Synthetic.
XX
PN      EP753581-A1.
XX
PD      15-JAN-1997.
XX
PF      10-JUL-1995; 95EP-0110727.
XX
PR      10-JUL-1995; 95EP-0110727.
XX
PA      (IMMO ) IMMUNO AG.
XX
PI      Antoine G, Dorner F, Eibl J, Falkner F, Scheiflinger F;
XX
DR      WPI; 1997-079382/08.
XX
PT      Prodn. of recombinant eukaryotic cytoplasmic DNA viruses for vaccine
PT      prodn. - using novel construct contg. foreign DNA and double
PT      selection marker
XX
PS      Example 9; Page 14; 68pp; English.
XX
CC      A method has been produced for the production of recombinant eukaryotic
CC      cytoplasmic DNA viruses for vaccine production. The method involves
CC      inserting a construct DNA molecule into the genome of a eukaryotic
CC      cytoplasmic DNA virus, transfecting cells with the virus, and selecting
CC      a recombinant virus that does not contain the double selection marker
CC      cassette from the construct DNA. The DNA molecule preferably contains
CC      one or more foreign DNA segments of a gene encoding an antigen of a
CC      pathogen (especially HIV env, HIV gag, HIV gagpol, HIV nef, HBV
CC      S surface antigen gene, HBV S1-S2-S surface antigen gene, HBV
CC      S surface antigen gene, tick-borne encephalitis prem gene or tick-borne
CC      encephalitis E gene), and has a double selection marker cassette which
CC      is flanked by at least two direct repeat DNA sequences, where at least
CC      one foreign DNA segment does not occur within the DNA sequence bounded
CC      by the direct repeat sequences and where the double selection marker
CC      cassette comprises a dominant selection marker gene and a colour
CC      selection marker gene (preferably the colour selection marker is the
CC      Escherichia coli lacZ gene and the dominant selection marker is the
CC      E.coli hph or gpt gene). The present sequence represents the oselp1
CC      oligonucleotide used in the construction of chimeric MVA vaccinia and
CC      fowlpox viruses expressing the tick-borne encephalitis virus prem and E
CC      genes. The DNA constructs and method are used for the production of
CC      vaccines, especially containing an attenuated live recombinant pox
CC      virus.
XX
SQ      Sequence 84 BP; 28 A; 8 C; 10 G; 38 T; 0 other;
Query Match 53.3%; Score 40; DB 18; Length 84;
Best Local Similarity 82.1%; Pred. No. 0.016;
Matches 46; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
RESULT 11
ID      AAT78341/C
XX
AC      AAT78341;
XX
DE      13-OCT-1997 (first entry)
XX
DE      Chimeric virus construction oligonucleotide oselp2.
XX
KM      Recombinant eukaryotic cytoplasmic DNA virus; vaccine production;
KM      double selection marker; attenuated live pox virus; HIV; HBV;
KM      surface antigen gene; encephalitis; tick-borne; ss.
XX
OS      Synthetic.
XX
PN      EP753581-A1.
XX
PD      15-JAN-1997.
XX
PF      10-JUL-1995; 95EP-0110727.
XX
PR      10-JUL-1995; 95EP-0110727.
XX
PA      (IMMO ) IMMUNO AG.
XX
PI      Antoine G, Dorner F, Eibl J, Falkner F, Scheiflinger F;
XX
DR      WPI; 1997-079382/08.
XX
PT      Prodn. of recombinant eukaryotic cytoplasmic DNA viruses for vaccine
PT      prodn. - using novel construct contg. foreign DNA and double
PT      selection marker
XX
PS      Example 9; Page 14; 68pp; English.
XX
CC      A method has been produced for the production of recombinant eukaryotic
CC      cytoplasmic DNA viruses for vaccine production. The method involves
CC      inserting a construct DNA molecule into the genome of a eukaryotic
CC      cytoplasmic DNA virus, transfecting cells with the virus, and selecting
CC      a recombinant virus that does not contain the double selection marker
CC      cassette from the construct DNA. The DNA molecule preferably contains
CC      one or more foreign DNA segments of a gene encoding an antigen of a
CC      pathogen (especially HIV env, HIV gag, HIV gagpol, HIV nef, HBV
CC      S surface antigen gene, HBV S1-S2-S surface antigen gene, HBV
CC      S surface antigen gene, tick-borne encephalitis prem gene or tick-borne
CC      encephalitis E gene), and has a double selection marker cassette which
CC      is flanked by at least two direct repeat DNA sequences, where at least
CC      one foreign DNA segment does not occur within the DNA sequence bounded
CC      by the direct repeat sequences and where the double selection marker
CC      cassette comprises a dominant selection marker gene and a colour
CC      selection marker gene (preferably the colour selection marker is the
CC      Escherichia coli lacZ gene and the dominant selection marker is the
CC      E.coli hph or gpt gene). The present sequence represents the oselp2
CC      oligonucleotide used in the construction of chimeric MVA vaccinia and
CC      fowlpox viruses expressing the tick-borne encephalitis virus prem and E
CC      genes. The DNA constructs and method are used for the production of
CC      vaccines, especially containing an attenuated live recombinant pox
CC      virus.
XX
SQ      Sequence 86 BP; 38 A; 11 C; 9 G; 28 T; 0 other;
Query Match 53.3%; Score 40; DB 18; Length 86;
Best Local Similarity 82.1%; Pred. No. 0.016;
Matches 46; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```



```

RESULT 12 '
AAZ46843/C
ID AAZ46843 standard; DNA; 78 BP.
XX
XX AAZ46843;
XX
XX 10-APR-2000 (first entry)
XX
XX Myxoma virus early/late promoter fragment generating oligo.
XX
XX Myxoma virus; CNCM I-1990; vaccine; myxomatosis; hemorrhagic disease;
XX rabbit; immunisation; promoter; ss.
XX
XX Myxoma virus.
XX
XX EP972840-A2.
XX
XX 19-JAN-2000.
XX
XX 10-JUN-1999; 99EP-0500099.
XX
XX 10-JUN-1998; 98ES-0001219.
XX
XX (PARA-) FUNDACION PARA EL ESTUDIO Y DEFENSA NATU.
XX (NAIN-) INST NACIONAL INVESTIGACION & TECNOLOGIA.
XX
XX Barcena DR, Blasco Lozano R, Morales Camarazana M, Pages Mante A;
XX Parra Fernandez F, Sanchez Vizcaino JM, Torres Trillo JM;
XX Vazquez Ruiz B;
XX
XX WPI; 2000-108130/10.
XX
XX Novel recombinant virus, used to treat myxomatosis and rabbit
XX hemorrhagic disease, in wild rabbits -
XX
XX Disclosure: Page 5; 29pp; English.
XX
XX The invention provides a recombinant myxoma virus deposited as
XX CNCM I-1990. The recombinant virus is used as a combined vaccine against
XX both myxomatosis and rabbit hemorrhagic disease, in wild rabbits. The
XX combined vaccine has a controlled self-propagating capacity which means
XX that not every animal needs to be individually immunized to get
XX efficient employment of the vaccine in wild rabbit populations. Sequences
XX AAZ46843-44 represent oligos for generating a myxoma virus early/late
XX promoter fragment.
XX
XX Sequence 78 BP; 30 A; 13 C; 9 G; 26 T; 0 other;
XX
XX Query Match 53.1%; Score 39.8; DB 21; Length 78;
XX Best Local Similarity 86.3%; Pred. No. 0.018; 7; Indels 0; Gaps 0;
XX Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
XX
OY 5 AAAAAATGAATTTATTTTGGAAATTAAGCGCGGCATG 55
Db 54 AAAAAATGAATTTATTTTGGAAATTAAGCGCGGCATG 4

RESULT 13
AAQ40300/C
ID AAQ40300 standard; DNA; 6474 BP.
XX
XX AAQ40300;
XX
XX 02-AUG-1993 (first entry)
XX
XX Sequence of plasmid pself-gp160MN.
XX
XX Plasmid; cloning; restriction site; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FH misc_feature 1..55

```

```

FT FT /tag- a
FT FT /label= pTZ19R
FT FT misc_feature complement (56..108)
FT FT /tag- b
FT FT /label= linker I in rc orientation
FT FT CDS complement (110..860)
FT FT /tag- c
FT FT /label= E. coli gpt
FT FT promoter complement (861..1245)
FT FT /tag- d
FT FT /label= Vaccinia virus p7.5
FT FT /note = "starting with the p7.5 internal NdeI site
FT FT at posn. 1241"
FT FT 1339..1344
FT FT /tag- e
FT FT /label= HpaI site
FT FT misc_feature complement (1259..3916)
FT FT /tag- f
FT FT /label= HIV-MN env gene
FT FT promoter complement (3917..3970)
FT FT /tag- g
FT FT /label= vaccinia virus synthetic early/late
FT FT promoter complement (3971..4015)
FT FT /tag- h
FT FT /label= linker II
FT FT misc_feature complement (4016..6474)
FT FT /tag- i
FT FT /label= pTZ19R
XX
XX AU9221269-A.
XX
XX 04-MAR-1993.
XX
XX 25-AUG-1992; 92AU-0021269.
XX
XX 26-AUG-1991; 91US-0750080.
XX PR 20-JUL-1992; 92US-0914738.
XX
XX (IMMO ) IMMUNO AG.
XX
XX Dörner F, Falkner FG, Pfeleiderer M, Schefflinger F;
XX WPI; 1993-126461/16.
XX
XX Modified eukaryotic cytoplasmic DNA virus prodn. - involves
XX PT direct molecular cloning of modified DNA molecule contg.
XX PT cytoplasmic DNA virus genome
XX
XX Example; Pages 169-172; 206pp; English.
XX
XX The synthetic early/late promoter self was used to express the
XX gp160-gene of the HIV-1 MN strain. For the construction of pL2
XX the 0.6kb XbaI-ClaI fragment of the plasmid pTM3 was substituted
XX by an XbaI-ClaI adaptor fragment consisting of the annealed
XX oligonucleotide 0-542 and 0-544. The intermediate plasmid
XX resulting from this cloning step was called pL1. The 0.4kb
XX AatII-SphI fragment were substituted by the AatII-SphI adaptor
XX fragment consisting of the annealed oligonucleotide 0-541 and
XX 0-543. The resulting plasmid was called pL2. The XbaI-SphI
XX fragment was treated with Klenow-polymerase and inserted between
XX the PvuII sites of the plasmid pTZ19R. The resulting plasmid was
XX called pTZ-L2. The 0.6kb ClaI-NcoI fragment (the T7-promoter-EKC-
XX sequence) was replaced with a synthetic promoter fragment
XX consisting of the annealed oligonucleotide 0-selfI and 0-selfPI.
XX The 239bp SalI-NdeI fragment of the resulting intermediate plasmid
XX was substituted by the SalI-NdeI adaptor consisting of the annealed
XX oligonucleotides 0-830 and 0-857. The resulting plasmid was called
XX pself-gpt-L2. The 3.1kb env gene containing the EcoRI-PvuII
XX fragment of pMNEV1 was inserted into the EcoRI and StuI cut plasmid
XX pself-gpt-L2 resulting in the intermediate plasmid pself-gp160.1.
XX The 0.8kb NcoI-NsiI fragment of pself-gp160 was substituted by a
XX PCR-generated 0.31kb NcoI-NsiI fragment resulting in the final
XX

```

CC plasmid pself-gp160MN. The primers used for the PCR reaction were
 CC o-NCOI and o-NSII.
 XX
 SQ Sequence 6474 BP; 1648 A; 1532 C; 1410 G; 1880 T; 4 other;

Query Match 52.8%; Score 39.6; DB 14; Length 6474;
 Best Local Similarity 83.3%; Pred. No. 0.048;
 Matches 45; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 5 AAAAATGAAATTTATTTTGGAAATATAAGCGCGCCCATGGGCC 58
 |||
 DB 3964 AAAAATGAAATTTATTTTGGAAATATAAGCGCCCATGGGCC 3911

RESULT 14
 AAA89877/C
 ID AAA89877 standard; DNA: 6474 BP.

XX AAA89877;

AC 26-JAN-2001 (first entry)

XX Plasmid pself-gp160 MN.

XX Vaccinia; fowlpox; virus; immune response; HIV; gp-160; gag;

KW gag-pol; ds.

XX Synthetic.

OS US6103244-A.

XX US6103244-A.

XX 15-AUG-2000.

XX 22-MAY-1996; 96US-0651472.

XX 19-DEC-1994; 94US-0358928.

XX 26-AUG-1991; 91US-0750080.

XX 20-JUL-1992; 92US-0914738.

XX (IMMO) IMMUNO AG.

XX Pfleiderer M, Falkner FG, Scheifflinger F, Dörner F;

XX WPI; 2000-557665/51.

XX Example 9; Column 147-154; 171pp; English.

CC The present invention relates to the use of modified vaccinia virus and
 CC fowlpox virus for generating or priming an immune response against a
 CC heterologous protein in a vertebrate. Suitable proteins include HIV
 CC proteins such as HIV gp160, HIV gag and HIV gag-pol proteins. The
 CC present sequence was associated with the generation or use of the
 CC modified viruses.

XX Sequence 6474 BP; 1649 A; 1533 C; 1411 G; 1881 T; 0 other;

Query Match 52.8%; Score 39.6; DB 21; Length 6474;

Best Local Similarity 83.3%; Pred. No. 0.048;
 Matches 45; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 5 AAAAATGAAATTTATTTTGGAAATATAAGCGCGCCCATGGGCC 58
 |||
 DB 3964 AAAAATGAAATTTATTTTGGAAATATAAGCGCCCATGGGCC 3911

RESULT 15
 AAS12795/C
 ID AAS12795 standard; DNA: 6474 BP.

AC AAS12795;
 XX
 DT 21-NOV-2001 (first entry)
 XX
 DE Plasmid pself-gp160MN DNA sequence.

XX Cytoplasmic DNA virus; direct molecular cloning; vaccinia virus; insect;
 KW unique restriction endonuclease cleavage site; infectious virion; ds;
 KM helper virus; poxvirus; iridovirus; vertebrate; multiple cloning site.

XX Synthetic.

XX US6265183-B1.

XX 24-JUL-2001.

XX 19-DEC-1994; 94US-0358928.

XX 26-AUG-1991; 91US-0750080.

XX 20-JUL-1992; 92US-0914738.

XX (BAXT) BAXTER AG.

XX Dörner F, Scheifflinger F, Falkner FG, Pfleiderer M;

XX WPI; 2001-535006/59.

XX Example 9; Column 149-154; 172pp; English.

CC The invention relates to a method for producing a modified eukaryotic
 CC cytoplasmic DNA virus by direct molecular cloning of a modified DNA
 CC molecule comprising a modified cytoplasmic DNA virus genome such as a
 CC vaccinia virus, containing a heterologous insert encoding a protein. The
 CC method involves molecularly cloning the DNA directly into a host cell via
 CC a unique restriction endonuclease cleavage site, to be packaged into
 CC infectious virions and then recovering them. The host cell is infected
 CC with a helper virus for this purpose. The method is useful for producing
 CC recombinant proteins and modified eukaryotic cytoplasmic DNA viruses such
 CC as poxviruses and iridoviruses found in vertebrates and insects. This
 CC sequence represents a plasmid pself-gp160MN used in the construction of
 CC chimeric vaccinia viruses.

XX Sequence 6474 BP; 1649 A; 1534 C; 1410 G; 1881 T; 0 other;

XX Query Match 52.8%; Score 39.6; DB 22; Length 6474;

Best Local Similarity 83.3%; Pred. No. 0.048;

Matches 45; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 5 AAAAATGAAATTTATTTTGGAAATATAAGCGCGCCCATGGGCC 58
 |||
 DB 3964 AAAAATGAAATTTATTTTGGAAATATAAGCGCCCATGGGCC 3911

Search completed: November 10, 2002, 05:58:25
 Job time : 90.4933 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:58:40 ; Search time 18.6657 Seconds

(Without alignments)
1425.554 Million cell updates/sec

Title: US-08-935-377-3

Perfect score: 75
Sequence: 1 GGCCAAAATGAAATTTTA.....GCCCGGCCCGCCACGCGGA 75

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 320260 seqs, 177392727 residues

Total number of hits satisfying chosen parameters: 640520

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PC1_NEM_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEM_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEM_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PC1_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEM_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEM_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEM_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEM_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	75	100.0	75	10	US-09-822-250-3
2	75	100.0	75	10	US-09-987-456-142
3	59	78.7	59	10	US-09-822-250-75
4	59	78.7	59	10	US-09-822-250-26
5	42.4	56.5	77	10	US-09-822-250-32
6	38.4	51.2	77	10	US-09-822-250-33
7	37	49.3	69	10	US-09-822-250-1
8	37	49.3	69	10	US-09-987-456-140
9	29.6	39.5	62944	10	US-09-954-456-2257
10	28	37.3	27483	10	US-09-764-877-2928
11	27.8	37.1	6855	10	US-09-764-864-1694
12	27.8	37.1	21045	10	US-09-764-864-1695
13	27.2	36.3	17784	10	US-09-764-877-3158
14	26.8	35.7	338	10	US-09-867-701-8272
15	26.8	35.7	468	10	US-09-969-373-257
16	26.8	35.7	584	12	US-10-001-879-21
17	26.8	35.7	1215	9	US-09-938-842A-1206
18	26.8	35.7	1905	9	US-09-938-842A-1193
19	26.8	35.7	3690	12	US-10-052-586-517

20	26.4	35.2	453	10	US-09-922-217-1047	Sequence 1047, Ap
21	26.4	35.2	453	10	US-09-833-263-1047	Sequence 1047, Ap
22	26.4	35.2	1172	10	US-09-764-869-1651	Sequence 1651, Ap
23	26.4	35.2	1172	10	US-09-764-869-1653	Sequence 1653, Ap
24	26.4	35.2	2000	9	US-09-938-842A-3467	Sequence 3467, Ap
25	26.2	34.9	31314	10	US-09-764-877-3875	Sequence 3875, Ap
26	26	34.7	2136	10	US-09-750-703-5	Sequence 5, Appl
27	26	34.7	84539	10	US-09-962-470-36	Sequence 36, Appl
28	25.8	34.4	240	10	US-09-878-574-7281	Sequence 7281, Ap
29	25.8	34.4	250	10	US-09-878-574-7255	Sequence 7255, Ap
30	25.8	34.4	553	10	US-09-864-761-13017	Sequence 13017, A
31	25.8	34.4	46718	10	US-09-816-093-3	Sequence 3, Appl1
32	25.6	34.1	95	10	US-09-864-761-18342	Sequence 18342, A
33	25.6	34.1	157	10	US-09-864-761-31398	Sequence 31398, A
34	25.6	34.1	355	10	US-09-960-352-14757	Sequence 14757, A
35	25.6	34.1	520	10	US-09-864-761-1584	Sequence 1584, Ap
36	25.6	34.1	470	10	US-09-864-761-14871	Sequence 14871, A
37	25.6	34.1	865	10	US-09-925-300-301	Sequence 301, App
38	25.4	33.9	180	10	US-09-815-343-734	Sequence 734, App
39	25.4	33.9	500	10	US-09-764-847-388	Sequence 388, App
40	25.4	33.9	4599	9	US-09-974-298-167	Sequence 167, App
41	25.4	33.9	32191	10	US-09-764-869-1955	Sequence 1955, Ap
42	25.2	33.6	425	10	US-09-834-975-451	Sequence 451, App
43	25.2	33.6	480	9	US-10-046-935-51	Sequence 51, Appl
44	25.2	33.6	2000	9	US-09-938-842A-3811	Sequence 3811, Ap
45	25.2	33.6	2000	10	US-09-887-576-135	Sequence 135, App

ALIGNMENTS

RESULT 1
US-09-822-250-3
Sequence 3, Application US/09822250
Patent NO. US2002018785A1
GENERAL INFORMATION:
APPLICANT: Zanderer, Maurice
TITLE OR INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
FILE REFERENCE: 1821.0010001
CURRENT FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: US 08/935,377
PRIOR FILING DATE: 1997-09-22
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 75
TYPE: DNA
ORGANISM: synthetic construct
FEATURE:
NAME/KEY: CDS
LOCATION: (52)..(75)
US-09-822-250-3

Query Match 100.0%; Score 75; DB 10; Length 75;
Best Local Similarity 100.0%; Pred. No. 2.3e-12;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCCAAAATGAAATTTATTTTGGATATATAAGCGCGCCATGCGCCG 60
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Db 1 GGCCAAAATGAAATTTATTTTGGATATATAAGCGCGCCATGCGCCG 60
61 GGCCGCAACGCGCGA 75
Db 61 GGCCGCAACGCGCGA 75

RESULT 2
US-09-987-456-142
Sequence 142, Application US/09987456
Patent NO. US20020123057A1
GENERAL INFORMATION:
APPLICANT: University of Rochester

```
; APPLICANT: Zauderer, Maurice
; APPLICANT: Ernest S. Smith
; TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
; FILE REFERENCE: 1821.0070004
; CURRENT APPLICATION NUMBER: US/09/987,456
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/271,424
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/262,067
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/298,087
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/249,268
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
; LENGTH: 75
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pe/Ltk promoter
; NAME/KEY: CDS
; LOCATION: (52)..(75)
; OTHER INFORMATION:
US-09-987-456-142

Query Match
Best Local Similarity 100.0%; Score 75; DB 10; Length 75;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGCAAAATTTGAATTTATTTTGGAAATATAAGCGCGCCCATGGCGCCG 60
DB 1 GGGCAAAATTTGAATTTATTTTGGAAATATAAGCGCGCCCATGGCGCCG 60
DB 61 GCGCCCAACGGCGGA 75
DB 61 GCGCCCAACGGCGGA 75

RESULT 3
US-09-822-250-25
; Sequence 25, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
; CURRENT APPLICATION NUMBER: US/09/822,250
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 59
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-822-250-25

Query Match
Best Local Similarity 78.7%; Score 59; DB 10; Length 59;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGCAAAATTTGAATTTATTTTGGAAATATAAGCGCGCCCATGGCGCC 59
DB 1 GGGCAAAATTTGAATTTATTTTGGAAATATAAGCGCGCCCATGGCGCC 59

RESULT 4
US-09-822-250-26/c
; Sequence 26, Application US/09822250
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; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
; CURRENT APPLICATION NUMBER: US/09/822,250
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 59
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-822-250-26

Query Match
Best Local Similarity 100.0%; Score 59; DB 10; Length 59;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 AAAAATTTGAATTTATTTTGGAAATATAAGCGCGCCCATGGCGCCG 63
DB 59 AAAAATTTGAATTTATTTTGGAAATATAAGCGCGCCCATGGCGCCG 63

RESULT 5
US-09-822-250-32
; Sequence 32, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
; CURRENT APPLICATION NUMBER: US/09/822,250
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 77
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-822-250-32

Query Match
Best Local Similarity 56.5%; Score 42.4; DB 10; Length 77;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGGCAAAATTTGAATTTATTTTGGAAATATAAGC 44
DB 1 GGGCAAAATTTGAATTTATTTTGGAAATATAAGC 44

RESULT 6
US-09-822-250-33/c
; Sequence 33, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
; CURRENT APPLICATION NUMBER: US/09/822,250
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 77
; TYPE: DNA
; ORGANISM: synthetic construct
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US-09-822-250-33

Query Match 51.2%; Score 38.4; DB 10; Length 77;
Best Local Similarity 97.5%; Pred. No. 0.022;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AAAAATGAAATTTATTTTATTTTGGAAATATAAAC 44
DB 77 AAAAATGAAATTTATTTTATTTTGGAAATATAAAC 38

RESULT 7

US-09-822-250-1
; Sequence 1, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
; CURRENT APPLICATION NUMBER: US/09/822,250
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 69
; TYPE: DNA
; ORGANISM: synthetic construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (46)..(69)
US-09-822-250-1

Query Match 49.3%; Score 37; DB 10; Length 69;
Best Local Similarity 78.7%; Pred. No. 0.051;
Matches 59; Conservative 0; Mismatches 10; Indels 6; Gaps 1;

QY 1 GCCCAAAATGAAATTTATTTTGGAAATATAAACGCCCGCATGGCCCG 60
DB 1 GCCCAAAATGAAATGAACTAGATCTATTATTTG-----CACGCGCGCGCATGGCCCG 54
QY 61 GCCGCAACGGCGGA 75
DB 55 GCCGCAACGGCGGA 69

RESULT 8

US-09-987-456-140
; Sequence 140, Application US/09987456.
; Patent No. US20020123057A1
; GENERAL INFORMATION:
; APPLICANT: University of Rochester
; APPLICANT: Zauderer, Maurice
; APPLICANT: Ernest S. Smith
; TITLE OF INVENTION: In Vitro Methods of Producing And Selecting
; FILE REFERENCE: 1821.0070004
; CURRENT APPLICATION NUMBER: US/09/987,456
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/271,424
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/262,067
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/298,087
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/249,268
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 140
; LENGTH: 69
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p7.5/tk promoter
; NAME/KEY: CDS
; LOCATION: (46)..(69)
; OTHER INFORMATION:
US-09-987-456-140

Query Match 49.3%; Score 37; DB 10; Length 69;
Best Local Similarity 78.7%; Pred. No. 0.051;
Matches 59; Conservative 0; Mismatches 10; Indels 6; Gaps 1;

QY 1 GCCCAAAATGAAATTTATTTTGGAAATATAAACGCCCGCATGGCCCG 60
DB 1 GCCCAAAATGAAATGAACTAGATCTATTATTTG-----CACGCGCGCGCATGGCCCG 54
QY 61 GCCGCAACGGCGGA 75
DB 55 GCCGCAACGGCGGA 69

RESULT 9

US-09-954-456-2257
; Sequence 2257, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2257
; LENGTH: 62944
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-2257

Query Match 39.5%; Score 29.6; DB 10; Length 62944;
Best Local Similarity 68.3%; Pred. No. 25;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 3 CCAAAATGAAATTTATTTTGGAAATATAAACGCCCGCATGGCCCG 62
DB 30903 CAAAGATATTAATTTCTTTTGGAAATGAGCTCACTCCATTGCCAGCC 30962

RESULT 10

US-09-764-877-2928
; Sequence 2928, Application US/09764877
; Patent No. US20020147140A1

```
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2928
; LENGTH: 27483
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2928

Query Match
Best Local Similarity 37.3%; Score 28; DB 10; Length 27483;
Matches 40; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 5 AAAAATTGAATTTATTTTATTTTGGATATATAAGCGCGCCATGGCGCCGCG 64
DB 25434 AACAAATGATTTTATTTTATTTTGGAGACAGAGTCTCCTCTGCGCCAGGCTG 25493

RESULT 11
US-09-764-1694/c
; Sequence 1694, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT23
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 1694
; LENGTH: 6855
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-1694

Query Match
Best Local Similarity 37.1%; Score 27.8; DB 10; Length 6855;
Matches 41; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 2 GCCAAATTTGAATTTTATTTTATTTTGGATATATAAGCGCGCCGATGGCGCG 61
DB 2411 GCCTAATTCATAAATCTTTTATTTTGGAGACAGAGTTCCTCATTCGCCAGG 2352

QY 62 CCG 64
DB 2351 CTG 2349

RESULT 12
US-09-764-1695
; Sequence 1695, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT23
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 1695
; LENGTH: 21045
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-09-764-1695

Query Match
Best Local Similarity 37.1%; Score 27.8; DB 10; Length 21045;
Matches 41; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 2 GCCAAATTTGAATTTTATTTTATTTTGGATATATAAGCGCGCCATGGCGCG 61
DB 18635 GCCTAATTCATAAATCTTTTATTTTGGAGACAGAGTTCCTCATTCGCCAGG 18694

QY 62 CCG 64
DB 18695 CTG 18697

RESULT 13
US-09-764-877-3158
; Sequence 3158, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 3158
; LENGTH: 17784
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3158

Query Match
Best Local Similarity 36.3%; Score 27.2; DB 10; Length 17784;
Matches 41; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GGCCAAATTTGAATTTTATTTTATTTTGGATATATAAGCGCGCCATGGCGCG 60
DB 1712 GGGAATATGAGATTTTATTTTGGAGATATGATCTCCTCTGTGCTAG 1771

QY 61 CCG 64
DB 1772 GCTG 1775

RESULT 14
US-09-867-701-8272/c
; Sequence 8272, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 8272
; LENGTH: 338
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-8272

Query Match
Best Local Similarity 35.7%; Score 26.8; DB 10; Length 338;
Matches 31; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 8 AATTGAATTTTATTTTATTTTATTTTGGATATATAAGCG 45
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Db 199 AATTAAATTTTGTGGAGACAGGG 162

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RESULT 15
; US-09-969-373-257
; Sequence 257, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Eifertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 257
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-257
    
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Query Match 35.7%; Score 26.8; DB 10; Length 468;
 Best Local Similarity 81.6%; Pred. No. 47;
 Matches 31; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 4 CAAAATTGAAATTTATTTTGGATATTA 41
 DB 246 CAAAATGATTTATTTTATTTTACTATTA 283

Search completed: November 10, 2002, 11:33:43
 Job time : 43.6657 secs

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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:43:30 ; Search time 19.2279 Seconds
(without alignments)
1196.219 Million cell updates/sec

Title: US-08-935-377-3

Perfect score: 75
Sequence: 1 GGCCAAAATTGAAATTTTA.....GCCCGCGCCGACGCGCGGA 75

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 segs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*
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3: /cgn2.6/ptodata/1/ina/6A.COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39.6	52.8	6474	US-08-651-472-66	Sequence 66, Appl
2	39.6	52.8	6474	US-08-358-928-66	Sequence 66, Appl
3	38.8	51.7	5532	US-08-651-472-72	Sequence 72, Appl
4	38.8	51.7	5532	US-08-358-928-72	Sequence 72, Appl
5	38.4	51.2	49	US-08-651-472-70	Sequence 70, Appl
6	38.4	51.2	49	US-08-358-928-70	Sequence 70, Appl
7	38.4	51.2	6811	US-08-651-472-67	Sequence 67, Appl
8	38.4	51.2	6811	US-08-358-928-67	Sequence 67, Appl
9	38.2	50.9	7252	US-09-238-356-27	Sequence 27, Appl
10	38.2	50.9	7387	US-09-238-356-28	Sequence 28, Appl
11	38	50.7	51	US-08-651-472-56	Sequence 56, Appl
12	38	50.7	51	US-08-358-928-56	Sequence 56, Appl
13	38	50.7	53	US-08-651-472-57	Sequence 57, Appl
14	38	50.7	53	US-08-358-928-57	Sequence 57, Appl
15	38	50.7	3878	US-08-651-472-65	Sequence 65, Appl
16	38	50.7	3878	US-08-358-928-65	Sequence 65, Appl
17	27.2	36.3	12597	US-09-705-289-12	Sequence 12, Appl
18	27	36.0	46	US-08-232-463-40	Sequence 40, Appl
19	27	36.0	63	US-08-232-463-47	Sequence 47, Appl
20	27	36.0	88	US-07-750-080A-11	Sequence 11, Appl
21	27	36.0	88	US-08-651-472-11	Sequence 11, Appl
22	27	36.0	88	US-08-358-928-11	Sequence 11, Appl
23	27	36.0	92	US-07-750-080A-12	Sequence 12, Appl
24	27	36.0	92	US-08-651-472-12	Sequence 12, Appl
25	27	36.0	92	US-08-358-928-12	Sequence 12, Appl
26	27	36.0	9890	US-08-232-463-18	Sequence 18, Appl
27	26.6	35.5	97	US-07-750-080A-41	Sequence 41, Appl

C 28	26.6	35.5	97	3	US-08-651-472-41	Sequence 41, Appl
C 29	26.6	35.5	97	4	US-08-358-928-41	Sequence 41, Appl
C 30	26.6	35.5	134	1	US-07-750-080A-14	Sequence 14, Appl
C 31	26.6	35.5	134	3	US-08-651-472-14	Sequence 14, Appl
C 32	26.6	35.5	134	4	US-08-358-928-14	Sequence 14, Appl
C 33	26.6	35.5	4145	3	US-08-651-472-62	Sequence 62, Appl
C 34	26.6	35.5	4145	4	US-08-358-928-62	Sequence 62, Appl
C 35	26	34.7	1000	2	US-08-747-121-20	Sequence 20, Appl
C 36	26	34.7	2002	2	US-08-747-121-1	Sequence 1, Appl
C 37	25.8	34.4	90	4	US-09-065-058-16	Sequence 16, Appl
C 38	25.6	34.1	785	4	US-09-185-244-9	Sequence 9, Appl
C 39	25.6	34.1	785	4	US-09-471-913-4	Sequence 4, Appl
C 40	25.6	34.1	1279	4	US-09-185-244-2	Sequence 2, Appl
C 41	25.6	34.1	1279	4	US-09-471-913-6	Sequence 6, Appl
C 42	25.4	33.9	3471	2	US-08-715-568A-2	Sequence 2, Appl
C 43	25.2	33.6	55	1	US-07-750-080A-38	Sequence 38, Appl
C 44	25.2	33.6	55	1	US-07-750-080A-39	Sequence 39, Appl
C 45	25.2	33.6	55	3	US-08-651-472-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-08-651-472-66/c
Sequence 66, Application US/08651472

Patent No. 6103244

GENERAL INFORMATION:

APPLICANT: DORNER, Friedrich

APPLICANT: SCHEFLINGER, Friedrich

APPLICANT: FALKNER, Falko Gunter

APPLICANT: FLEIDERER, Michael

TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC

TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1

NUMBER OF SEQUENCES: 95

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM: disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/651,472

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/914,738

FILING DATE: 20-JUL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/750,080

FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 30472/166/IMMU

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 66:

SEQUENCE CHARACTERISTICS:

LENGTH: 6474 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid:

DESCRIPTION: Synthetic DNA oligonucleotide
IMMEDIATE SOURCE:
CLONE: psc1p-9p160M
US-08-651-472-66

Query Match 52.8%; Score 39.6; DB 3; Length 6474;
Best Local Similarity 83.3%; Pred. No. 0.0032;
Matches 45; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 5 AAAAATGAAATTTATTTTGTGGAATATAAGCGCGCCATGGGCC 58
|||||
Db 3964 AAAAATGAAATTTATTTTGTGGAATATAAGCGCCATGGGCC 3911

RESULT 2
US-08-358-928-66/c
Sequence 66, Application US/08358928

GENERAL INFORMATION:
APPLICANT: DORNER, Friedrich
APPLICANT: SCHEFLINGER, Friedrich
APPLICANT: FALKNER, Falko Gunter
APPLICANT: FLEIDERER, Michael
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
NUMBER OF INVENTIONS: (HIV-1) ANTIGENS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358, 928
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914, 738
FILING DATE: 20-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/750, 080
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/166/IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 6474 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
IMMEDIATE SOURCE:
CLONE: psc1p-9p160M
US-08-358-928-66

Query Match 52.8%; Score 39.6; DB 4; Length 6474;
Best Local Similarity 83.3%; Pred. No. 0.0032;
Matches 45; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 5 AAAAATGAAATTTATTTTGTGGAATATAAGCGCGCCATGGGCC 58
|||||
Db 3964 AAAAATGAAATTTATTTTGTGGAATATAAGCGCCATGGGCC 3911

RESULT 3
US-08-651-472-72/c
Sequence 72, Application US/08651472
Patent No. 6103244

GENERAL INFORMATION:
APPLICANT: DORNER, Friedrich
APPLICANT: SCHEFLINGER, Friedrich
APPLICANT: FALKNER, Falko Gunter
APPLICANT: FLEIDERER, Michael
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
NUMBER OF INVENTIONS: (HIV-1) ANTIGENS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,472
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,738
FILING DATE: 20-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/750,080
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/166/IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 72:

SEQUENCE CHARACTERISTICS:
LENGTH: 5532 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
IMMEDIATE SOURCE:
CLONE: pN29p1a-FIX
US-08-651-472-72

Query Match 51.7%; Score 38.8; DB 3; Length 5532;
Best Local Similarity 79.3%; Pred. No. 0.0053;
Matches 46; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 3 CCAAATGAAATTTATTTTGTGGAATATAAGCGCGCCATGGGCCG 60
|||||
Db 3709 CTAATAATGAAATTTATTTTGTGGAATATAAGCGCCATGGACG 3652

RESULT 4
US-08-358-928-72/c
Sequence 72, Application US/08358928
Patent No. 6265183

```

GENERAL INFORMATION:
APPLICANT: DORNER, Friedrich
APPLICANT: SCHEIFLINGER, Friedrich
APPLICANT: FALKNER, Falko Gunter
APPLICANT: PLEIDERER, Michael
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
TITLE OF INVENTION: (HIV-1) ANTIGENS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,928
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,738
FILING DATE: 20-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/750,080
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/166/IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 5532 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
IMMEDIATE SOURCE:
CLONE: PN29pta-FIX
US-08-358-928-72

Query Match          51.7%; Score 38.8; DB 4; Length 5532;
Best Local Similarity 79.3%; Pred. NO. 0.0053;
Matches 46; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 3 CCAAAATGGAATTTTATTTTGGATATTAAGCGCGCCATGGCGCCG 60
DB 3709 CTAATAATGGAATTTTATTTTGGATATTAAGCGCTCCATGGAGCG 3652

RESULT 5
US-08-651-472-70
Sequence 70, Application US/08651472
Patent No. 6103244
GENERAL INFORMATION:
APPLICANT: DORNER, Friedrich
APPLICANT: SCHEIFLINGER, Friedrich
APPLICANT: FALKNER, Falko Gunter
APPLICANT: PLEIDERER, Michael
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
TITLE OF INVENTION: (HIV-1) ANTIGENS
NUMBER OF SEQUENCES: 95
```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,472
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,738
FILING DATE: 20-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/750,080
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/166/IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
IMMEDIATE SOURCE:
CLONE: self promoter
US-08-651-472-70

Query Match          51.2%; Score 38.4; DB 3; Length 49;
Best Local Similarity 97.5%; Pred. NO. 0.0022;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCAAAATGGAATTTTATTTTGGATATTA 42
DB 9 CTAATAATGGAATTTTATTTTGGATATTA 48

RESULT 6
US-08-358-928-70
Sequence 70, Application US/08358928
Patent No. 6265183
GENERAL INFORMATION:
APPLICANT: DORNER, Friedrich
APPLICANT: SCHEIFLINGER, Friedrich
APPLICANT: FALKNER, Falko Gunter
APPLICANT: PLEIDERER, Michael
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
TITLE OF INVENTION: (HIV-1) ANTIGENS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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1  COMPUTER: IBM PC compatible
2  OPERATING SYSTEM: PC-DOS/MS-DOS
3  SOFTWARE: Patentin Release #1.0, Version #1.30
4  CURRENT APPLICATION DATA:
5  APPLICATION NUMBER: US/08/358,928
6  FILING DATE:
7  CLASSIFICATION: 435
8  PRIOR APPLICATION DATA:
9  APPLICATION NUMBER: US 07/914,738
10 FILING DATE: 20-JUL-1992
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: US 07/750,080
13 FILING DATE: 26-AUG-1991
14 ATTORNEY/AGENT INFORMATION:
15 NAME: BENT, Stephen A.
16 REGISTRATION NUMBER: 29,768
17 REFERENCE/DOCKET NUMBER: 30472/166/1MMU
18 TELECOMMUNICATION INFORMATION:
19 TELEPHONE: (202)672-5300
20 TELEFAX: (202)672-5399
21 TELEX: 904136
22 INFORMATION FOR SEQ ID NO: 70:
23 SEQUENCE CHARACTERISTICS:
24 LENGTH: 49 base pairs
25 TYPE: nucleic acid
26 STRANDEDNESS: single
27 TOPOLOGY: linear
28 MOLECULE TYPE: other nucleic acid:
29 DESCRIPTION: Synthetic DNA oligonucleotide
30 IMMEDIATE SOURCE:
31 CLONE: self promoter
32 US-08-358-928-70

```

Query Match	51.2%	Score 38.4	DB 4	Length 49
Best Local Similarity	97.5%	Pred. No. 0.0022		
Matches 39; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	3	CCAAAAATTGAATTTTATTTTTTTTTTTGGCAATATAA	42	
db	9	CTAAAAATTGAATTTTATTTTTTTTTTTGGCAATATAA	48	

RESULT 7
 US-08-651-472-67/c
 Sequence 67, Application US/08651472
 Patent No. 6103244
 GENERAL INFORMATION:
 APPLICANT: DORNER, Friedrich
 APPLICANT: SCHEIFLINGER, Friedrich
 APPLICANT: FALKNER, Falko Gunter
 APPLICANT: PLEIDERER, Michael
 TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
 TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
 NUMBER OF SEQUENCES: 95
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/651,472
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/914,738

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1      FILING DATE: 20-JUL-1992
2      PRIOR APPLICATION DATA:
3      APPLICATION NUMBER: US 07/750, 080
4      FILING DATE: 26-AUG-1991
5      ATTORNEY/AGENT INFORMATION:
6      NAME: BENT, Stephen A.
7      REGISTRATION NUMBER: 29, 768
8      REFERENCE/DOCKET NUMBER: 304772/166/IMKU
9      TELECOMMUNICATION INFORMATION:
10     TELEPHONE: (202)672-5300
11     TELEFAX: (202)672-5399
12     TELEX: 904136
13
14     INFORMATION FOR SEQ ID NO: 67:
15     SEQUENCE CHARACTERISTICS:
16     LENGTH: 6811 base pairs
17     TYPE: nucleic acid
18     STRANDEDNESS: single
19     TOPOLOGY: linear
20     MOLECULE TYPE: Other nucleic acid:
21     DESCRIPTION: Synthetic DNA oligonucleotide
22     IMMEDIATE SOURCE:
23     CLONE: pN2-gpca Prots
24
25     JS-08-651-472-67

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Query Match:	51.2%	Score 38.4;	DB 3;	Length 6811;
Overall Similarity	97.5%	Pred. No. 0.0074;		
Best Local Match:				
Matches 33;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	3	CCAAAAATGAAATTTATTTTTTTTTTGGATATATAA	42	
db	4388	CTAAAAATGAAATTTATTTTTTTTTTGGAAATATAA	4949	

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```

;
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6811 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid;
; DESCRIPTION: Synthetic DNA oligonucleotide
; IMMEDIATE SOURCE:
; CLONE: pN2-9pla Prots
;
US-08-358-928-67

Query Match
Best Local Similarity 97.5%; Score 38.4; DB 4; Length 6811;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 CCAAAATGAAATTTATTTTGGAAATATAA 42
Db 4988 CTAATAATGAAATTTATTTTGGAAATATAA 4949

RESULT 9
US-09-238-356-27/c
; Sequence 27, Application US/09238356
; Patent No. 6312683
; GENERAL INFORMATION:
; APPLICANT: Kingsman, et al
; TITLE OF INVENTION: Retroviral Vectors
; FILE REFERENCE: 674523-2006
; CURRENT APPLICATION NUMBER: US/09/238,356
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: PCT/GB/03876
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 7252
; TYPE: DNA
; ORGANISM: Artificial Sequence, plasmid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(7252)
; OTHER INFORMATION: plasmid vector
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AX003206
; DATABASE ENTRY DATE: 2000-08-24
; RELEVANT RESIDUES: (1)..(7252)
;
US-09-238-356-27

Query Match
Best Local Similarity 93.0%; Score 38.2; DB 4; Length 7252;
Matches 40; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 AAAAATGAAATTTATTTTGGAAATATAAGCGGC 47
Db 874 AAAAATGAAATTTATTTTGGAAATATAAGC 832

RESULT 10
US-09-238-356-28/c
; Sequence 28, Application US/09238356
; Patent No. 6312683
; GENERAL INFORMATION:
; APPLICANT: Kingsman, et al
; TITLE OF INVENTION: Retroviral Vectors
; FILE REFERENCE: 674523-2006
; CURRENT APPLICATION NUMBER: US/09/238,356
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: PCT/GB/03876
; PRIOR FILING DATE: 1998-12-22
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;
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 7387
; TYPE: DNA
; ORGANISM: Artificial Sequence, primer
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(7387)
; OTHER INFORMATION: plasmid vector
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AX003207
; DATABASE ENTRY DATE: 2000-08-24
; RELEVANT RESIDUES: (1)..(7387)
;
US-09-238-356-28

Query Match
Best Local Similarity 93.0%; Score 38.2; DB 4; Length 7387;
Matches 40; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 AAAAATGAAATTTATTTTGGAAATATAAGCGGC 47
Db 3889 AAAAATGAAATTTATTTTGGAAATATAAGC 3847

RESULT 11
US-08-651-472-56
; Sequence 56, Application US/08651472
; Patent No. 6103244
; GENERAL INFORMATION:
; APPLICANT: DORNER, Friedrich
; APPLICANT: SCHEIFLINGER, Friedrich
; APPLICANT: FALKNER, Falko Gunter
; APPLICANT: FEIDERER, Michael
; TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
; TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
; TITLE OF INVENTION: (HIV-1) ANTIGENS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; City: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/651,472
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/914,738
; FILING DATE: 20-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/750,080
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/166/JMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```

TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
IMMEDIATE SOURCE:
CLONE: o-selp1
US-08-651-472-56

Query Match 50.7%; Score 38; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AAAAATTGAATTTATTTTGGAAATATAA 42
|||||
DB 5 AAAAATTGAATTTATTTTGGAAATATAA 42

RESULT 12

US-08-358-928-56
Sequence 56, Application US/08358928
Patent No. 6265183

GENERAL INFORMATION:
APPLICANT: DORNER, Friedrich
APPLICANT: SCHEFFLINGER, Friedrich
APPLICANT: FALKNER, Falko Gunter
APPLICANT: PLEIDERER, Michael
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,928
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,738
FILING DATE: 20-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/750,080
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/166/IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
TELEFAX: 904136
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
IMMEDIATE SOURCE:
CLONE: o-selp1
US-08-358-928-56

Query Match 50.7%; Score 38; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.003;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 AAAAATTGAATTTATTTTGGAAATATAA 42
|||||
DB 5 AAAAATTGAATTTATTTTGGAAATATAA 42

RESULT 13

US-08-651-472-57/c
Sequence 57, Application US/08651472
Patent No. 6103244

GENERAL INFORMATION:
APPLICANT: DORNER, Friedrich
APPLICANT: SCHEFFLINGER, Friedrich
APPLICANT: FALKNER, Falko Gunter
APPLICANT: PLEIDERER, Michael
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,472
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,738
FILING DATE: 20-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/750,080
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/166/IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 53 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
IMMEDIATE SOURCE:
CLONE: o-selp1
US-08-651-472-57

Query Match 50.7%; Score 38; DB 3; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AAAAATTGAATTTATTTTGGAAATATAA 42
|||||
DB 51 AAAAATTGAATTTATTTTGGAAATATAA 14

RESULT 14
US-08-358-928-57/c

```
; Sequence 57, Application US/08358928
; Patent No. 6265183
; GENERAL INFORMATION:
; APPLICANT: DORNER, Friedrich
; APPLICANT: SCHEIFLINGER, Friedrich
; APPLICANT: FALKNER, Falko Gunter
; APPLICANT: FLEIDERER, Michael
; TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
; TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,928
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/914,738
; FILING DATE: 20-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/750,080
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/166/IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid;
; DESCRIPTION: Synthetic DNA oligonucleotide
; IMMEDIATE SOURCE:
; CLONE: o-selpII
;
US-08-358-928-57

Query Match 50.7%; Score 38; DB 4; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AAAAATGAAATTTATTTTTCGAAATATATA 42
Db 51 AAAAATGAAATTTATTTTTCGAAATATATA 14

RESULT 15
US-08-651-472-65/C
; Sequence 65, Application US/08651472
; Patent No. 6103244
; GENERAL INFORMATION:
; APPLICANT: DORNER, Friedrich
; APPLICANT: SCHEIFLINGER, Friedrich
; APPLICANT: FALKNER, Falko Gunter
; APPLICANT: FLEIDERER, Michael
; TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
; TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/651,472
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/914,738
; FILING DATE: 20-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/750,080
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/166/IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3878 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid;
; DESCRIPTION: Synthetic DNA oligonucleotide
; IMMEDIATE SOURCE:
; CLONE: pselp-gpt-L2
;
US-08-651-472-65

Query Match 50.7%; Score 38; DB 3; Length 3878;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AAAAATGAAATTTATTTTTCGAAATATATA 42
Db 1368 AAAAATGAAATTTATTTTTCGAAATATATA 1331
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; TITLE OF INVENTION: (HIV-1) ANTIGENS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/651,472
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/914,738
; FILING DATE: 20-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/750,080
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/166/IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3878 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid;
; DESCRIPTION: Synthetic DNA oligonucleotide
; IMMEDIATE SOURCE:
; CLONE: pselp-gpt-L2
;
US-08-651-472-65

Query Match 50.7%; Score 38; DB 3; Length 3878;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AAAAATGAAATTTATTTTTCGAAATATATA 42
Db 1368 AAAAATGAAATTTATTTTTCGAAATATATA 1331
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Search completed: November 10, 2002, 08:36:09
Job time : 26.2279 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run On: November 10, 2002, 05:05:45 ; Search time 705 Seconds

(without alignments)
5985.683 Million cell updates/sec

Title: US-08-935-377-6

Perfect score: 145

Sequence: 1 GGCAGAAATGAAACTA.....TTGTTTGTGGCCCGCC 145

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sls:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
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23: em_pat:*
24: em_ph:*
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27: em_scs:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	145	100.0	145	6 AX326743	AX326743 Sequence
2	132	91.0	148	6 AX326744	AX326744 Sequence
3	131	90.3	149	6 AX326745	AX326745 Sequence
4	130	89.7	150	6 AX326746	AX326746 Sequence
5	70.8	48.8	4326	12 AF072997	AF072997 Cloning v
6	70.4	48.6	5255	12 AF309793	AF309793 Clupea pa
7	70.4	48.6	5592	6 AR205969	AR205969 Sequence
8	70.2	48.4	656	5 AF309795	AF309795 Clupea pa
9	69.4	47.9	13558	6 AX287041	AX287041 Sequence
10	69	47.6	259	6 AX284796	AX284796 Sequence
11	69	47.6	424	6 AX34154	AX34154 Cloning v
12	69	47.6	2059	12 AB035274	AB035274 Homo sap1
13	69	47.6	2890	6 AX247548	AX247548 Sequence
14	69	47.6	2958	12 ARBLKSM	X53326 pbuescript
15	69	47.6	2958	12 ARBLKSP	X53327 pbuescript
16	69	47.6	2958	12 ARBLKSP	X53329 pbuescript
17	69	47.6	2961	12 ARBL2KSM	X53327 pbuescript
18	69	47.6	2961	12 ARBL2KSP	X53327 pbuescript
19	69	47.6	2964	12 SYNBLSKSPV	L06784 Bluescribe
20	69	47.6	2964	12 SYNBLSKSPV	L06784 Bluescribe
21	69	47.6	306	12 SYNBLSKSPV	D85525 Cloning vec
22	69	47.6	3417	12 AF153422	AF153422 Cloning v
23	69	47.6	3485	12 AF178449	AF178449 Integrati
24	69	47.6	4144	12 X035131	U35131 Plasmid pbs
25	69	47.6	4267	12 PRS304	U03436 Yeast integ
26	69	47.6	4289	12 X035136	U35136 Plasmid pbs
27	69	47.6	4373	12 PRS306	U03438 Yeast integ
28	69	47.6	4443	12 PRS303	U03435 Yeast integ
29	69	47.6	4549	12 AF178452	AF178452 Integrati
30	69	47.6	4670	12 ASAJ5326	AJ005326 pGAL1(+)
31	69	47.6	4670	12 ASAJ5329	AJ005329 pGAL1(-)
32	69	47.6	4707	12 X002374	U02374 Cloning vec
33	69	47.6	4768	12 X0025061	U25061 Cloning vec
34	69	47.6	4783	12 PRS314	U03440 Yeast cent
35	69	47.6	4887	12 PRS316	U03442 Yeast cent
36	69	47.6	4950	12 X025060	U25060 Cloning vec
37	69	47.6	4967	12 PRS313	U03439 Yeast cent
38	69	47.6	5144	12 CV023751	U23751 Cloning vec
39	69	47.6	5187	12 U34887	U34887 Yeast integ
40	69	47.6	5228	12 X025059	U25059 Cloning vec
41	69	47.6	5504	12 PRS305	U03437 Yeast integ
42	69	47.6	5634	12 CV014125	U14125 Cloning vec
43	69	47.6	5973	12 AF504908	AF504908 Cloning v
44	69	47.6	6018	12 PRS315	U03441 Yeast cent
45	69	47.6	6340	12 ASAJ5323	AJ005323 pCP1(-) K

ALIGNMENTS

RESULT 1
AX326743 145 bp DNA linear PAT 07-JAN-2002
LOCUS AX326743
DEFINITION Sequence 4 from Patent WO0172995.
ACCESSION AX326743
VERSION AX326743.1 GI.18097469
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct.
artificial sequences.
REFERENCE
1
Zaenderer, M. and Smith, E. S.
Methods of producing a library and methods of selecting
polynucleotides of interest
Patent: WO 0172995-A 4 04-OCT-2001.
JOURNAL

UNIVERSITY OF ROCHESTER (US)
FEATURES Location/Qualifiers
SOURCE 1.145
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Nucleotide Sequence of p7.5/ATG0/Lk"
BASE COUNT 34 a 37 c 38 g 36 t
ORIGIN

Query Match 100.0%; Score 145; DB 6; Length 145;
Best Local Similarity 100.0%; Pred. No. 8e-36;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGCAAAATTTGAAAACCTAGATCTATTATTTGACAGCGCGCGCGCGATCCCGCGGC 60
|||||
DB 1 GGGCAAAATTTGAAAACCTAGATCTATTATTTGACAGCGCGCGCGCGATCCCGCGGC 60
|||||

OY 61 TGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCTAACTAAC 120
|||||
DB 61 TGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCTAACTAAC 120
|||||

OY 121 TAATTTTGTGTTTGTGGCGCGCGC 145
|||||
DB 121 TAATTTTGTGTTTGTGGCGCGCGC 145
|||||

RESULT 2
AX326744 148 bp DNA linear PAT 07-JAN-2002
LOCUS
DEFINITION Sequence 5 from Patent WO0172995.
ACCESSION AX326744
VERSION AX326744.1 GI:18097470
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Zauderer,M. and Smith,E.S.
TITLE Methods of producing a library and methods of selecting
JOURNAL polynucleotides of interest
UNIVERSITY OF ROCHESTER (US)
FEATURES Location/Qualifiers
SOURCE 1.148
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Nucleotide Sequence of p7.5/ATG1/Lk"
BASE COUNT 35 a 37 c 39 g 37 t
ORIGIN

Query Match 91.0%; Score 132; DB 6; Length 148;
Best Local Similarity 98.0%; Pred. No. 1.2e-31;
Matches 145; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

OY 1 GGGCAAAATTTGAAAACCTAGATCTATTATTTGACAGCGCGCGCGCGATCCCGCGGC 57
|||||
DB 1 GGGCAAAATTTGAAAACCTAGATCTATTATTTGACAGCGCGCGCGCGATCCCGCGGC 60
|||||

OY 58 GGGTCGAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCTAACT 117
|||||
DB 61 GGGTCGAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCTAACT 120
|||||

OY 118 AACTAATTTTGTGTTTGTGGCGCGCGC 145
|||||
DB 121 AACTAATTTTGTGTTTGTGGCGCGCGC 148
|||||

RESULT 3
AX326745 149 bp DNA linear PAT 07-JAN-2002
LOCUS
DEFINITION Sequence 6 from Patent WO0172995.
ACCESSION AX326745
VERSION AX326745.1 GI:18097471

KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Zauderer,M. and Smith,E.S.
TITLE Methods of producing a library and methods of selecting
JOURNAL polynucleotides of interest
UNIVERSITY OF ROCHESTER (US)
FEATURES Location/Qualifiers
SOURCE 1.149
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Nucleotide Sequence of p7.5/ATG2/Lk"
BASE COUNT 36 a 37 c 39 g 37 t
ORIGIN

Query Match 90.3%; Score 131; DB 6; Length 149;
Best Local Similarity 97.3%; Pred. No. 2.5e-31;
Matches 145; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

OY 1 GGGCAAAATTTGAAAACCTAGATCTATTATTTGACAGCGCGCGCGCGATCCCGCGGC 56
|||||
DB 1 GGGCAAAATTTGAAAACCTAGATCTATTATTTGACAGCGCGCGCGCGATCCCGCGGC 60
|||||

OY 57 GGGTCGAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCTAACT 116
|||||
DB 61 GGGTCGAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCTAACT 120
|||||

OY 117 TAACATAATTTTGTGTTTGTGGCGCGCGC 145
|||||
DB 121 TAACATAATTTTGTGTTTGTGGCGCGCGC 149
|||||

RESULT 4
AX326746 150 bp DNA linear PAT 07-JAN-2002
LOCUS
DEFINITION Sequence 7 from Patent WO0172995.
ACCESSION AX326746
VERSION AX326746.1 GI:18097472
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Zauderer,M. and Smith,E.S.
TITLE Methods of producing a library and methods of selecting
JOURNAL polynucleotides of interest
UNIVERSITY OF ROCHESTER (US)
FEATURES Location/Qualifiers
SOURCE 1.150
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Nucleotide Sequence of p7.5/ATG3/Lk"
BASE COUNT 36 a 38 c 39 g 37 t
ORIGIN

Query Match 89.7%; Score 130; DB 6; Length 150;
Best Local Similarity 96.7%; Pred. No. 5.3e-31;
Matches 145; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

OY 1 GGGCAAAATTTGAAAACCTAGATCTATTATTTGACAGCGCGCGCGCGATCCCGCGGC 55
|||||
DB 1 GGGCAAAATTTGAAAACCTAGATCTATTATTTGACAGCGCGCGCGCGATCCCGCGGC 60
|||||

OY 56 GGGTCGAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCTAACT 115
|||||
DB 61 GGGTCGAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCTAACT 120
|||||

OY 116 CTAACATAATTTTGTGTTTGTGGCGCGCGC 145
|||||

D6		121	CTAACTAATTGTTTGTGGCCGCCGCC	150
RESULT 5				
LOCUS	AF072997			
DEFINITION	AE072997	4326 bp	DNA	circular SYN 02-JUL-1998
ACCESSION	Cloning vector pCMWTA33a,			complete sequence.
VERSION	AF072997			
KEYWORDS	AF072997..1 GI:3284001			
SOURCE				
ORGANISM	Cloning vector pCMWTA33a.			
REFERENCE	Cloning vector pCMWTA33a			
AUTHORS	artificial sequences; vectors.			
TITLE	1 (bases 1 to 4326)			
JOURNAL	Lu.O.			
REFERENCE	Unpublished			
AUTHORS	2 (bases 1 to 4326)			
TITLE	Lu.O.			
JOURNALS	Direct Submission			
FEATURES	Submitted (22-JUN-1998) Technical Services, Stratagene, 1101 N. Torrey Pines Rd., San Diego, CA 92037, USA Location/Qualifiers			
source	1..4326	/organism="Cloning vector pCMWTA33a"		
promoter	/db_xref="taxon:78249" /lab_host="Escherichia coli K12"			
misc.feature	1..602	/note="CMV promoter"		
misc.feature	713..799	/note="multiple cloning site"		
misc.feature	859..1242	/note="SV40 polyA signal region"		
rep.origin	1242..1703	/note="f1 origin of replication"		
promoter	1704..1835	/note=".Pbla promoter"		
rep.origin	1836..2227	/note="SV40 origin of replication"		
CDS	2228..3022	/function="kanamycin resistance"		
		/codon_start=1		
		/transl_table=1		
		/product="aminoglycoside phosphotransferase"		
		/protein_id="AAC25426.1"		
		/db_xref="GI:3284002"		
		/translation="MIRDDGLHAGSPAAWERLFGYMAOITTCSDAAVRLSAQGRF PVLFVKTDLSGALNELDEAKRSLWLMTTGPCAVIDVTYEAGRDIILLGEVGQDIL LSSHLPAEKVISLMADMRRLHTLDPTCPDHAKRIERAPTRMEAGVLVDODDLDEE EHQIOLAPAELEFARKASMPDGEDLVTVHGACLPIINVENRGFSFGTDCGRIVADRHY QDIDLATRIAEEELGSEWMADRFVLVYGIAAPDSQRIFARLLDFEF"		
	3469..4316			
BASE COUNT	1056 a 1116 c 1107 g 1047 t			
ORIGIN				
Query Match	48.8%; Score 70.8; DB 12;			
Best Local Similarity	76.3%; Pred. No. 8.9e-12;			
Matches	87; Conservative 0; Mismatches 27; Indels 0; Gaps 0;			
OY	12 GAATAACTAGATCTATTATTGCAGCGCGCGCGCATCCCCGGCGCTGCAGAATTC	71		
Db	681 GCAGAACTCATTCTGAAGAGGATCTCCCGCGGCGGAGATCCC CGGCGCTGCAGGAATTC	740		
OY	72 GATATCAAGCTTATGATACGCTGACCTGCAGGGGGGGCTAACTACTAATT	125		
Db	741 GATATCAAGCTTATGATACCGCTGACCTGCAGGGGGGGCCGGTACCTTAATT	794		
RESULT 6				
LOCUS	AF309793/c	525 bp	DNA	linear VRT 23-JAN-2002
DEFINITION	Alupea pallasi microsatellite Chai13 sequence.			

ACCESSION	AF309793
VERSION	AF309793.1 GI:12060921
KEYWORDS	
SOURCE	
ORGANISM	Clupea pallasi.
	Clupea pallasi
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;
	Clupea.
REFERENCE	1 (bases 1 to 525)
AUTHORS	Miller,K.M., Laboree,K., Schulze,A.D. and Kaukinen,K.H.
TITLE	Development of microsatellite loci in Pacific herring (<i>Clupea</i>
JOURNAL	pallasi)
FEATURES	Mol. Ecol. Notes 1 (3), 131-132 (2001)
source	2 (bases 1 to 525)
	Miller,K.M., Laboree,K. and Kaukinen,K.
	Direct Submission
	Submitted (02-OCT-2000) Aquaculture/Genetics, Pacific Biological
	Station, Hammond Bay Rd., Nanaimo, B.C. V9R 5K6, Canada
	location/Qualifiers
	1..525
	/organism="Clupea pallasi"
	/db_xref="taxon:30724"
	/clone="Cha113"
repeat_region	1..525
	/note="microsatellite Cha113"
	/rpl_type=landem
BASE COUNT	130 a 136 c 166 g 93 t
ORIGIN	
Query Match	48.6%; Score 70.4; DB 5; Length 525;
Best Local Similarity	79.8%; Pred. No. 8,7e-12;
Matches	83; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
OY	27 TTATTTGCAGCCGGCGCCGTGATCCCCCGGGCTGCAGATTGATATCAAGCTTATC 86
Db	126 TTGCATGAGACACCAGCACAGATCCCCGGCGCTGCAGATTGATATCAAGCTTATC 67
OY	87 GATAACGTCGACTCGAGGGGGGCCCTAATTAATTTTGT 130
Db	66 GATACCGTCGACTCGAGGGGGGCCAGTACCAAGCTTTGTT 23
RESULT 7	
LOCUS	AR205969 5592 bp DNA linear PAT 20-JUN-2002
DEFINITION	Sequence 37 from patent US 6369296.
ACCESSION	AR205969
VERSION	AR205969.1 GI:21503686
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 5592)
	Ratcliff,F.Giles., Martin-Hernandez,A.Montserrat. and
	Baulcombe,D.Charles.
TITLE	Recombinant plant viral vectors
JOURNAL	Patent: US 6369296-A 37 09-APR-2002;
FEATURES	location/Qualifiers
source	1..5592
	/organism="unknown"
BASE COUNT	1517 a 1318 c 1276 g 1481 t
ORIGIN	
Query Match	48.6%; Score 70.4; DB 6; Length 5592;
Best Local Similarity	79.8%; Pred. No. 1,2e-11;
Matches	83; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
OY	9 ATTGAANAATCATATTTATTTCACAGCGCGCCGTGATCCCCCGGGCTGCAGAA 68
Db	2514 ATTTAAGAGACTGAACCTGTGTGAGATCCTGAAGACTAGTGATGCCCGGGCTGCAGAA 2573
OY	69 TTGCATATCAAGCTTATCGATACCGTCGACTCGAGGGGGGCC 112

FEATURES	
SOURCE	Location/Qualifiers
	1. .424
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
BASE COUNT	87 a 134 c 118 g 85 t
ORIGIN	

Query Match	47.6%	Score 69	DB 6	Length 424
Best Local Similarity	88.2%	Pred. No. 2.4e-11		
Matches	75	Conservative	0	Mismatches 10; Indels 0; Gaps 0
QY	46	GTGGATCCCCCGGCTGCAGAAATCGAATCAACTTATGATACCGTGCACCTGAGG	105	
Db	104	GTGATATCCCCCGGCTGCAGAAATCGAATCAACTTATGATACCGTGCACCTGAGG	45	
QY	106	GGGGGCTTAACCTAATATTTGTT	130	
Db	44	GGGGGCTTAACCTAATATTTGTT	20	

RESULT 12			
LOCUS AY034154/c			
DEFINITION Cloning vector pIDM4, complete sequence.	2059 bp	DNA	circular SYN 23-JUL-2001
ACCESSION AY034154			
VERSION AY034154.1	GI:14324126		
KEYWORDS			
ORGANISM			
SOURCE			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MI			
FEATURES			
source			
promoter			
promoter			
stem_loop			
gene			
CDS			
AY034154			
Cloning vector pIDM4, complete sequence.			
AY034154			
AY034154.1	GI:14324126		
Cloning vector pIDM4.			
Cloning vector pIDM4.			
artificial sequences: vectors.			
1 (bases 1 to 2059)			
Hamilton,H.L., Schwartz,K.J. and Dillard,J.P.			
Insertion-duplication mutagenesis of neisseria: use in			
characterization of DNA transfer genes in the gonococcal genetic			
island			
J. Bacteriol. 183 (16), 4718-4726 (2001)			
21359313			
11466274			
2 (bases 1 to 2059)			
Hamilton,H.L., Schwartz,K.J. and Dillard,J.P.			
Direct Submision			
Submitted (11-MAY-2001) Medical Microbiology & Immunology,			
University of Wisconsin-Madison, 1300 University Avenue, Madison,			
WI 53706 USA			
Location/Qualifiers			
1..2059			
/organism="Cloning vector pIDM4"			
/db_xref="taxon:161273"			
/note="for Insertion-duplication mutagenesis in Neisseria"			
40..59			
/note="r3"			
complement(187..204)			
/note="r7"			
277..311			
complement(310..1113)			
/gene="ermC"			
complement(310..1044)			
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/codon_start=1			
/transl_table=11			
/product="ErmC"			
/protein_id="AAK58461.1"			
/db_xref="GI:14324127"			
/translation="MNEKNIKHSQNFITTSKHNDKIMPTNIRLNEHONIFEIGSGRGHF			
TLELVORCFVTAIEIDHKLKCTENKLVDHDNQVLNKDIILOFKPKQSYKINGNI			
PVIISDTDIRKIIVFSIADDELYLIVEGFARLRINTRSALFLMAEVDISLSWPR			
EYHPKPYNSSILIRLNKKSRISHKDKOKRYNVPMKWVKKEKKIFTTNGQNSNISKH			
AGCIDDNNTSPFOFSLFNYSKLFNK"			
complement(1051..1054)			
/gene="ermC"			
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complement(1086..1091)			
/gene="ermC"			
complement(1108..1113)			
/gene="ermC"			
1130..1139			
/note="DNA uptake sequence (DUS)"			
complement(1145..1154)			
/note="DNA uptake sequence (DUS)"			
complement(1276..1976)			

		/note="RNA II"	
		complement(1422.. .1423)	
	-rep_origin	1830.. .1835	
	-35_signal	1859.. .1865	
	-10_signal	1854.. .1859	
	misc_RNA	1866.. .1973	
		/note="RNA I"	
	-10_signal	complement(1984.. .1989)	
	-35_signal	complement(2007.. .2012)	
BASE COUNT	566 a	452 c	424 g
ORIGIN		617 t	
Query Match	47.6%; Score 69;	DB 12; Length 2059;	
Best Local Similarity	88.2%; Pred. No. 3e-11;		
Matches 75; Conservative	0; Mismatches 10; Indels	0; Gaps	0;
QY	46 GTGATCCCCCGGGGTGCAGAAATTCGAATCAACCTAATCAGTAAACCGTGACTCGAGG	105	
Dd	143 GTGATCCCCCGGGGTGCAGAAATTCGAATCAACCTAATCAGTAAACCGTGACTCGAGG	84	
OY	106 GGGGCCCTAACCTAATTGTTT	130	
Dd	83 GGGGGCCCGGTACCAGCTTTT	59	

RESULT	13
LOCUS	AB035274
DEFINITION	AB035274 2890 bp mRNA linear PRI 12-JUL-2000
ACCESSION	Hom sapiens mRNA for postreplication repair protein hRad18p, complete cds.
VERSION	AB035274
KEYWORDS	AB035274.1 GI:8980616
SOURCE	Hom sapiens placenta cDNA to mRNA.
ORGANISM	Hom sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (sites)
REFERENCE	Tateishi,S., Sakuraba,Y., Masuyama,S., Inoue,H. and Yamatzumi,M. Dysfunction of human Rad18 results in defective postreplication repair and hypersensitivity to multiple mutagens Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7927-7932 (2000) 20345089
JOURNAL	2 (bases 1 to 2890)
MEDLINE	Tateishi,S., Yamatzumi,M. and Inoue,H. Direct Submission
REFERENCE	Institute of Molecular Biology, Kumamoto University, Kumamoto 862-0976, Japan (E-mail:tateisgo.kumamoto-u.ac.jp, Tel.81-096-373-6602, Fax:81-096-373-6604)
AUTHORS	Location/Qualifiers
JOURNAL	1..2890
FEATURES	/organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="3" /tissue_type="placenta"
source	1..2890 /gene="hRad18" 126..1613 /gene="hRad18" /note="RING-zinc-finger protein" /codon_start=1 /product="postreplication repair protein hRad18p" /protein_id="BA099284.1" /db_xref="GI:8980617" /translation="MDSLAEHWMPGLAVMKTTIDLLRGICIEFYENIAMITPQCSHN TGLCLRKFLSTKTCPCVCYVVEPDKNRRLIDELVKSLNFARNHLLOPLLESPAK SPASSSKNLAAVYTVPAASLSSKOGSRIMDNLIRESGSTSELLIKENKSRSPO SEAPSAKTETRSVEETIADPPSEAKREPPESTDLKYOVKDCPGVGYNIPESHNK HLDSLCISREKKESLSRSSVHKRRPLPTKVNNLLSDRLKKKLKEHGLSTGKKOLIL RDIEFHHYNAQCDAHLHPKSAAEIVOEIENESTRMLETASKINESWVFYTDOTEKE IDIEHSKRYKKKSEFOLLNDQARKGYRTKIAGSQRYVTTKDESTEKLSSVCGOE DNMTSYTNHFSSKDFEELEPREDDSSCIDIOEVASSSDSCNSSSSDIIRLL LEPERAWESNRNDIQDTETISPQRNRRRAAESNAETPRNKRNRN"
gene	
CDS	

```

BASE COUNT      916 a      585 c      601 g      788 t
ORIGIN
Query Match      47.6%; Score 69; DB 9; Length 2890;
Best Local Similarity 88.2%; Pred. No. 3.2e-11;
Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 46 GTGATCCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 105
    |||||||
DB 2742 GTGATCCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 2801
    |||||||

QY 106 GGGGGCCTTAACCTAATTTTGT 130
    |||||||
DB 2802 GGGGGCCTTAACCTAATTTTGT 2826
    |||||||

RESULT 14
AX247548      2958 bp      DNA      linear      PAT 28-SEP-2001
LOCUS
DEFINITION Sequence 1 from Patent WO0166775.
ACCESSION AX247548
VERSION AX247548.1 GI:15862240
KEYWORDS
SOURCE
ORGANISM synthetic construct.
          artificial sequences.
REFERENCE 1 (bases 1 to 2958)
AUTHORS Evans,D.H., Willer,D.O. and Yao,X.D.
TITLE Dna joining method
JOURNAL Patent: WO 0166775-A 1 13-SEP-2001;
          University of Guelph (CA)
FEATURES
    source
        1..2958
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /note="pDW101"

BASE COUNT      748 a      735 c      752 g      723 t
ORIGIN
Query Match      47.6%; Score 69; DB 6; Length 2958;
Best Local Similarity 88.2%; Pred. No. 3.2e-11;
Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 46 GTGATCCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 105
    |||||||
DB 684 GTGATCCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 743
    |||||||

QY 106 GGGGGCCTTAACCTAATTTTGT 130
    |||||||
DB 744 GGGGGCCTTAACCTAATTTTGT 768
    |||||||

RESULT 15
ARBLKSM      2958 bp      DNA      circular SYN 29-JAN-2002
LOCUS
DEFINITION pBluescript KS(-) vector DNA, phagemid excised from lambda ZAP.
ACCESSION X52326
VERSION X52326.1 GI:58064
KEYWORDS artificial sequence; cloning vector; expression vector; vector.
SOURCE
ORGANISM synthetic construct.
          synthetic construct.
          artificial sequences.
REFERENCE 1
AUTHORS Short,J.M., Fernandez,J.M., Sorge,J.A. and Huse,W.D.
TITLE Lambda ZAP: a bacteriophage lambda expression vector with in vivo
          excision properties
JOURNAL Nucleic Acids Res. 16 (15), 7583-7600 (1988)
MEDLINE 90067967
PUBMED 2555794
REFERENCE 3 (bases 1 to 2958)
AUTHORS Thomas,E.A.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-1990) Thomas E.A., Stratagene Clonin Systems,
          11099 North Torrey Pines Rd., La Jolla, CA 92037, USA
FEATURES
    source
        1..2958
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /note="phagemid pBluescript KS(-)"
        misc_feature
            1..2958
                /note="phagemid pBluescript KS(-)"

BASE COUNT      708 a      754 c      731 g      765 t
ORIGIN
Query Match      47.6%; Score 69; DB 12; Length 2958;
Best Local Similarity 88.2%; Pred. No. 3.2e-11;
Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 46 GTGATCCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 105
    |||||||
DB 687 GTGATCCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 746
    |||||||

QY 106 GGGGGCCTTAACCTAATTTTGT 130
    |||||||
DB 747 GGGGGCCTTAACCTAATTTTGT 771
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Search completed: November 10, 2002, 06:52:54
Job time : 713 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:42:15 ; Search time 1305 Seconds

(without alignments)
1799,499 Million cell updates/sec

Title: US-08-935-377-6

Sequence: 1 GGCCAAAATGAAAACTA.....TTGTTTGTGGCCGCCGCC 145

Scoring table: IDENTITY-NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75.4	52.0	891	14	B0140386 NF035A10P
2	72	49.7	182	13	B1306115 NL_3_G09
3	72	49.7	793	14	B0143916 B0143916
4	70.4	48.6	841	17	CNS06W11 AL417851 T7 end of
5	70	48.3	536	17	CNS06VAH AL416895 T7 end of
6	70	48.3	682	17	AQ074693 CIT-HSP-2

7	69.8	48.1	804	14	B0158468	B0158468 NF058H09P
8	69.6	48.0	355	17	CNS06XBT	AL419535 T7 end of
9	69.4	47.9	182	13	B1305962	B1305962 NL_2_K23
10	69.4	47.9	186	13	B1305695	B1305695 NL_1_G23
11	69.2	47.7	574	17	BH001110	BH001110 G139 Germ
12	69.2	47.7	912	17	CNS06UFS	AL415767 T7 end of
13	69	47.6	162	10	BE428068	BE428068 MT0002.H1
14	69	47.6	390	9	AU234451	AU234451 AU234451
15	69	47.6	400	9	AU278852	AU278852 AU278852
16	69	47.6	864	17	AQ937400	AQ937400 NB2-011.H
17	68.8	47.4	175	13	B1306167	B1306167 NL_3_J08
18	68.8	47.4	182	13	B1306149	B1306149 NL_3_I07
19	68.8	47.4	182	13	B1306159	B1306159 NL_3_I22
20	68.8	47.4	182	13	B1306178	B1306178 NL_3_K05
21	68.8	47.4	182	13	B1306180	B1306180 NL_3_K07
22	68.8	47.4	757	14	B0155148	NF076G11I
23	68	46.9	295	10	BE428455	BE428455 MT0007.CO
24	68	46.9	608	17	AQ009167	AQ009167 CIT-HFP-2
25	67.8	46.8	728	10	AM682547	AM682547 EST01410
26	67.6	46.6	216	17	CNS06E50	AL394690 T7 end of
27	67.6	46.6	829	17	AQ937397	AQ937397 NB2-006.H
28	67.4	46.5	128	17	CNS07GJ4	AL609826 Anopheles
29	67.4	46.5	528	17	B69688	B69688 CIT976SK-A-
30	67.4	46.5	721	17	CNS06DOU	AL394084 T7 end of
31	67.4	46.5	902	17	CNS06W0M	AL418916 T7 end of
32	67.2	46.3	198	17	CNS06X0I	AL419128 T7 end of
33	67.2	46.3	968	17	CNS06V41	AL416663 T7 end of
34	67	46.2	107	13	BM398556	BM398556 5009-0-47
35	67	46.2	108	10	BE492551	BE492551 WHE0554.C
36	67	46.2	108	17	B54292	B54292 CIT-HSP-201
37	67	46.2	124	10	AW914179	AW914179 EST345483
38	67	46.2	141	9	AU037147	AU037147 AU037147
39	67	46.2	141	17	B95279	B95279 CIT-HSP-217
40	67	46.2	144	17	B80294	B80294 CIT-HSP-204
41	67	46.2	157	12	BF281431	BF281431 EST446022
42	67	46.2	169	13	B1306719	B1306719 NL_5_N23
43	67	46.2	169	17	AQ013255	AQ013255 CIT-HSP-2
44	67	46.2	175	17	AQ041198	AQ041198 CIT-HSP-2
45	67	46.2	180	13	B1306345	B1306345 NL_4_E10

ALIGNMENTS

RESULT 1
LOCUS B0140386
DEFINITION NF035A10PHJ1081 Phoma-infected Medicago truncatula cDNA clone
ACCESSION B0140386
VERSION B0140386.1 GI:20276512
KEYWORDS
SOURCE
ORGANISM
barel medic.
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
1 (bases 1 to 891)
Watson,B.S., Shin,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R.,
Gonzales,R.A., Bell,C.J., Imman,J.T., Waugh,M.E., Sullivan,J.P.,
May,G.D. and Paiva,N.L.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula Phoma-infected library
Unpublished (2002)
Contact: Paiva NL
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7317
Fax: 580 221 7380
Email: nlpaiva@noble.org
Insert Length: 891 Std Error: 0.00

Plate: 035 row: A column: 10
Seq primer: TCACACAGGAACAGCTATGAC.
Location/Qualifiers

FEATURES

source

1. .891
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF035A10PH"
/clone_lib="Phoma-Infected"
/tissue_type="leaf"
/dev_stage="Pathogen-induced, young trifoliolate"
/note="Vector: Bluescript SK(-); Young trifoliolate leaves of Medicago truncatula were excised and dip-inoculated in a spore suspension of Phoma medicaginis, and incubated in humid dishes. Pools of leaves were harvested at 0, 15, and 30 minutes and 1, 2, 3, 6, 14, 24, 48, 72, and 96, hours, and used to prepare total RNA. cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directionally ligated into the Uni-zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-ZAP XR vector using ExAssist helper phage and the E. coli strain XL1-Blue MR⁺ (Stratagene). Excised plasmids were plated using SOUT cells."

BASE COUNT 188 a 151 c 64 g 224 t 264 others
ORIGIN

Query Match 52.0%; Score 75.4; DB 14; Length 891;
Best Local Similarity 87.8%; Pred. No. 7.6e-15;
Matches 79; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 46 GTGATCCCCCGGCTGCAGATTCGATATCAAGCTTATGATACCGCTGCAGG 105
|||||
DB 84 GTGATCCCCCGGCTGCAGATTCGATATCAAGCTTATGATACCGCTGCAGG 143
QY 106 GGGGCGCTAATCTAATTTGTTTGT 135
|||||
DB 144 GGGGCGCGGTATCTATTTTCTATNT 173

RESULT 2
BI306115/c 182 bp mRNA linear EST 20-JUL-2001
LOCUS NL_3 G09 Drought stress (leaf) Oryza sativa cDNA clone NL_3_G09 3',
DEFINITION mRNA sequence.
ACCESSION BI306115
VERSION BI306115.1 GI:14981437
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 182)
Reddy A.R., Ramakrishna W., Chandrasekhar A., Nagabushan, I.,
Ravindrababu, P. and Bennetzen, J. L.
Novel EST enrichment with normalized cDNA libraries from drought
stressed rice (Oryza sativa L. cv Nagina 22)
Unpublished (2001)
Contact: Reddy AR
Department of Plant Sciences, School of Life Sciences
University of Hyderabad
P.O. Central university, Hyderabad-500 046, A.P., India
Tel: 0091-40-3010265
Fax: 0091-40-3010145
Email: arjuls@uohyd.ernet.in
Insert length: 182 Std Error: 0.00
Plate: 3 row: G column: 09
Seq primer: GTAAACGACGGCCACATG.
Location/Qualifiers

JOURNAL COMMENT
source
1. .182
/organism="Oryza sativa"

FEATURES

source

1. .182
/organism="Oryza sativa"

/cultivar="Nagina 22 (indica sub sp.)"
/db_xref="taxon:4530"
/clone="NL_3_G09"
/clone_lib="Drought stress (leaf)"
/tissue_type="Entire leaf tissue"
/dev_stage="35 day-old seedlings"
/note="Organ: leaf; Vector: T7T3Pac; ESTs from normalized leaf cDNA library from drought stressed seedlings"

BASE COUNT 34 a 47 c 53 g 48 t
ORIGIN

Query Match 49.7%; Score 72; DB 13; Length 182;
Best Local Similarity 93.8%; Pred. No. 1e-13;
Matches 75; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 46 GTGATCCCCCGGCTGCAGATTCGATATCAAGCTTATGATACCGCTGCAGG 105
|||||
DB 107 GTGATCCCCCGGCTGCAGATTCGATATCAAGCTTATGATACCGCTGCAGG 48
QY 106 GGGGCGCTAATCTAATTT 125
|||||
DB 47 GGGGCGCGGTATCTATTTTCTATNT 28

RESULT 3
B0143916 793 bp mRNA linear EST 24-APR-2002
LOCUS NF038H04D1F1041 Drought Medicago truncatula cDNA clone NF038H04D
DEFINITION 5', mRNA sequence.
ACCESSION B0143916
VERSION B0143916.1 GI:20280975
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
1 (bases 1 to 793)
Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula drought library
Unpublished (2000)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert length: 793 Std Error: 0.00
Plate: 038 row: H column: 04
Seq primer: TCACACAGGAACAGCTATGAC.
Location/Qualifiers

FEATURES

source

1. .793
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF038H04D"
/clone_lib="Drought"
/tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
/note="Vector: lambda zap; Contains a mixture of entire plantlets harvested in a series of days-post-watering timepoints."

BASE COUNT 217 a 203 c 205 g 168 t
ORIGIN

Query Match 49.7%; Score 72; DB 14; Length 793;
Best Local Similarity 93.8%; Pred. No. 1.1e-13;
Matches 75; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 46 GTGATCCCCCGGCTGCAGATTCGATATCAAGCTTATGATACCGCTGCAGG 105

Db	85	GTCGATCCCGGGGTGCAGGAATTGCATATCAGACTTATCATACCGTGACCTCGAGG	144
Oy	106	GGGGCCTTACTAATAATT	125
Db	145	GGGGGCCCGAGTACCATAATT	164
RESULT 4			
LOCUS	CNS06M11	841 bp	DNA linear GSS 06-JUL-2001
DEFINITION	T7 end of clone AX0AA027B04 of library AX0AA from strain CBS 7064		
ACCESSION	AL417851		
VERSION	ALA17851.1		
KEYWORDS	GI:12200086		
SOURCE			
ORGANISM	Pichia farinosa.		
REFERENCE	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia.		
AUTHORS	1 (bases 1 to 841) Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bojotin-Fukuhara,M., Bon,E., Brotier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durieux,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,M., Tekala,F., Toffano-Nioche,C., Weslowski-Louvel,M., Winkler,P. and Weissenbach,J. Genomic exploration of the hemiascomycetous yeasts: I. A set of yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000)		
TITLE			
JOURNAL			
MEDLINE	20584771		
PUBMED	11152876		
REFERENCE	2 (bases 1 to 841) de Montigny,J., Spehner,C., Souciet,J., Tekala,F., Dujon,B., Winkler,P., Artiguenave,F. and Potier,S. Genomic exploration of the hemiascomycetous yeasts: 15. Pichia sorbitophila FEBS Lett. 487 (1), 87-90 (2000)		
AUTHORS			
TITLE			
JOURNAL			
MEDLINE	20584725		
PUBMED	11152890		
REFERENCE	3 (bases 1 to 841) Genoscope.		
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
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PUBMED			
REFERENCE			
AUTH			

Db	728	TACCTAGACGACGAGATGACGAGATGCCCGGGCTTCAGAGATTGCATATCAAGCTTA	787
QY	85	TCGATACCGTCGACCTCGAGGGGGGCC	112
Db	788	TCGATACCGTCGACCTCGAGGGGGGCC	815
RESULT 5			
CNS06VAH			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
REFERENCE			
AUTHORS			
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MEDLINE			
PUBMED			

OY 95 CGACCTCGAGGGGGGCC 112
DB 485 CGACCTCGAGGGGGGCC 502

RESULT 6
LOCUS A0074693/c
DEFINITION CIT-HSP-2301L23.TF CIT-HSP Homo sapiens genomic clone 2301L23, DNA
sequence.
ACCESSION A0074693
VERSION A0074693.1 GI:3436811
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 682)
Adams,M.D., Rounsley,S.D., Zhao,S., Baas,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.
AUTHORS Venter,J.C.
TITLE Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
JOURNAL Unpublished (1998)
COMMENT Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES
source location/Qualifiers
1..682
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2301L23"
/clone_1id="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelobAC1; site_1: HindIII; site_2:
HindIII"

BASE COUNT 156 a 187 c 187 g 151 t 1 others
ORIGIN

Query Match 48.3%; Score 70; DB 17; Length 682;
Best Local Similarity 93.6%; Pred. No. 5.2e-13;
Matches 72; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 46 GTGATCTCCCCGGGCTGCGAATTCATATCAAGCTTATGATACCGTGCACCTCGAG 105
DB 78 GTGATCTCCCCGGGCTGCGAATTCATATCAAGCTTATGATACCGTGCACCTCGAG 19

OY 106 GGGGGCTTAACCTAA 123
DB 18 GGGGGCTCGAGTACC 1

RESULT 7
LOCUS B0158468
DEFINITION B0158468 804 bp mRNA linear EST 24-APR-2002
clone NF058H09PL 5', mRNA sequence.
ACCESSION B0158468
VERSION B0158468.1 GI:20295525
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula

REFERENCE
AUTHORS Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 804)
TITLE
JOURNAL
COMMENT Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mjharrison@noble.org
Insert Length: 804 Std Error: 0.00
Plate: 058 row: H column: 09
Seq primer: TCACACGAGAAACGCTATGAC.

FEATURES
source location/Qualifiers
1..804
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF058H09PL"
/clone_1id="phosphate starved leaf"
/tissue_type="leaf"
/dev_stage="trifoliolate"
/note="Vector: Lambda Zap; At the trifoliolate stage, M.
truncatula plants were transplanted to phosphate-free sand
and grown for a further 30 days. During this 30 day
period, the plants were fertilized twice weekly with 1/2
Hoaglands solution containing only 20uM potassium
phosphate. RNA was prepared from above ground tissues."

BASE COUNT 215 a 202 c 181 g 165 t 41 others
ORIGIN

Query Match 48.1%; Score 69.8; DB 14; Length 804;
Best Local Similarity 89.2%; Pred. No. 6.1e-13;
Matches 74; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 46 GTGATCTCCCCGGGCTGCGAATTCATATCAAGCTTATGATACCGTGCACCTCGAG 105
DB 82 GTGATCTCCCCGGGCTGCGAATTCATATCAAGCTTATGATACCGTGCACCTCGAG 141

OY 106 GGGGGCTTAACCTAA 128
DB 142 GGGGGCTGTRACCAATTC 164

RESULT 8
LOCUS CNS06XBT
DEFINITION CNS06XBT 355 bp DNA linear GSS 06-JUL-2001
T7 end of clone XAX0A001B07 of library XAX0A from strain CBS 7064
of Pichia farinosa, genomic survey sequence.
ACCESSION AL419535
VERSION AL419535.1 GI:12202713
KEYWORDS GSS.
SOURCE Pichia farinosa.
ORGANISM Pichia farinosa.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.
REFERENCE Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Boulotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Duret,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvéglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Douvet,M.,
Wincker,P. and Weissbach,J.
TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711

PUBMED 11152876
 REFERENCE 2 (bases 1 to 355)
 AUTHORS de Montigny J., Spehner C., Souciet J., Tekala F., Dujon B., Wincker P., Artiguenave F. and Potier S.
 TITLE Genomic exploration of the hemiascomycetous yeasts: 15. *Pichia sorbitophila*
 JOURNAL FEBS Lett. 487 (1), 87-90 (2000)
 MEDLINE 20584725
 PUBMED 11152890
 REFERENCE 3 (bases 1 to 355)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr Web : www.genoscope.cns.fr)
 COMMENT This GSS is part of a random genomic sequencing program of thirteen yeast species: *Saccharomyces bayanus* var. *uvaurum*, *Saccharomyces exiguus*, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
 FEATURES Location/Qualifiers
 source 1..355
 /organism="Pichia farinosa"
 /strain="CBS 7064"
 /db_xref="taxon:4920"
 /clone="XAX0A001B07"
 /clone_1id="XAX0A"
 /note="end : T7"
 BASE COUNT 64 a 91 c 109 g 86 t 5 others
 ORIGIN
 Query Match 48.0%; Score 69.6; DB 17; Length 355;
 Best Local Similarity 92.3%; Pred. No. 6.9e-13;
 Matches 72; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 35 ACGGCGCCGCGTGATGCCCGGGGCTGCAGAAATTCGATCAAGCTTATCGATTACCGT 94
 Db 242 ACTGCGCGCTGCTGATGCCCGGGGCTGCAGAAATTCGATCAAGCTTATCGATTACCGT 301
 QY 95 CGACCTCGAGGGGGGCC 112
 Db 302 CGACCTCGAGGGGGGCC 319
 RESULT 9
 BI305962/c 182 bp mRNA linear EST 20-JUL-2001
 LOCUS NL_2_K23 Drought stress (leaf) Oryza sativa cDNA clone NL_2_K23 3', mRNA sequence.
 ACCESSION BI305962
 VERSION BI305962.1 GI:14981284
 KEYWORDS EST.
 SOURCE Oryza sativa.
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 182)
 AUTHORS Reddy A.R., Ramakrishna W., Chandrasekhar A., Nagabhushan I., Ravindrababu P. and Bennetzen J.L.
 TITLE Novel EST enrichment with normalized cDNA libraries from drought stressed rice (*Oryza sativa* L. cv Nagina 22)
 JOURNAL Unpublished (2001)
 COMMENT Contact: Reddy AR
 Department of Plant Sciences, School of Life Sciences
 University of Hyderabad
 P.O. Central University, Hyderabad-500 046, A.P., India
 Tel: 0091-40-3010265

Fax: 0091-40-3010145
 Email: arjuls@uohyd.ernet.in
 Insert Length: 182 Std Error: 0.00
 Plate: 2 row: K column: 23
 Seq primer: GTTAAACGACGGCCAGTG.
 FEATURES Location/Qualifiers
 source 1..182
 /organism="Oryza sativa"
 /cultivar="Nagina 22 (indica sub sp)"
 /db_xref="taxon:4530"
 /clone="NL_2_K23"
 /clone_1id="Drought stress (leaf)"
 /tissue_type="Entire leaf tissue"
 /dev_stage="35 day-old seedlings"
 /note="Organ: Leaf; Vector: T7T3Pac; ESTs from normalized leaf cDNA library from drought stressed seedlings"
 BASE COUNT 34 a 48 c 52 g 46 t 2 others
 ORIGIN
 Query Match 47.9%; Score 69.4; DB 13; Length 182;
 Best Local Similarity 91.2%; Pred. No. 7.9e-13;
 Matches 73; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 46 GTGATCCCCCGGCGTGCAGAAATTCGATCAAGCTTATCGATTACCGTCGACCTGAGG 105
 Db 107 GTGATCCCCCGGCGTGCAGAAATTCGATCAAGCTTATCGATTACCGTCGACCTGAGG 48
 QY 106 GGGGCGCTTAATCAATAT 125
 Db 47 GGGGCGCCGCTACCAAT 28
 RESULT 10
 BI305695/c 186 bp mRNA linear EST 20-JUL-2001
 LOCUS NL_1_G23 Drought stress (leaf) Oryza sativa cDNA clone NL_1_G23 3', mRNA sequence.
 ACCESSION BI305695
 VERSION BI305695.1 GI:14981017
 KEYWORDS EST.
 SOURCE Oryza sativa.
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 186)
 AUTHORS Reddy A.R., Ramakrishna W., Chandrasekhar A., Nagabhushan I., Ravindrababu P. and Bennetzen J.L.
 TITLE Novel EST enrichment with normalized cDNA libraries from drought stressed rice (*Oryza sativa* L. cv Nagina 22)
 JOURNAL Unpublished (2001)
 COMMENT Contact: Reddy AR
 Department of Plant Sciences, School of Life Sciences
 University of Hyderabad
 P.O. Central University, Hyderabad-500 046, A.P., India
 Tel: 0091-40-3010265
 Fax: 0091-40-3010145
 Email: arjuls@uohyd.ernet.in
 Insert Length: 186 Std Error: 0.00
 Plate: 1 row: G column: 23
 Seq primer: GTTAAACGACGGCCAGTG.
 FEATURES Location/Qualifiers
 source 1..186
 /organism="Oryza sativa"
 /cultivar="Nagina 22 (indica sub sp)"
 /db_xref="taxon:4530"
 /clone="NL_1_G23"
 /clone_1id="Drought stress (leaf)"
 /tissue_type="Entire leaf tissue"
 /dev_stage="35 day-old seedlings"
 /note="Organ: Leaf; Vector: T7T3Pac; ESTs from normalized leaf cDNA library from drought stressed seedlings"
 BASE COUNT 35 a 47 c 56 g 46 t 2 others

ORIGIN

Query Match 47.9%; Score 69.4; DB 13; Length 186;
 Best Local Similarity 91.2%; Pred. No. 7.9e-13;
 Matches 73; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 46 GTGATCCCGGGGCTGACGAATTCGATTCAGCTTATCGATTACCGTCGACCTGAGG 105
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 DB 111 GTGATCCCGGGGCTGACGAATTCGATTCAGCTTATCGATTACCGTCGACCTGAGG 52
 |||

QY 106 GGGGCTACTACTAATTT 125
 |||
 DB 51 GGGGGCNCGGTACCCCAATT 32
 |||

RESULT 11
 BH001110

LOCUS 574 bp DNA linear GSS 01-JUL-2001

DEFINITION G139 Gemmata obscuriglobus phagemid library Gemmata obscuriglobus genomic clone G139 similar to cadmium efflux system accessory protein, DNA sequence.

ACCESSION BH001110 GI:14579876

VERSION BH001110

KEYWORDS GSS.

SOURCE Gemmata obscuriglobus.

ORGANISM Gemmata obscuriglobus
 Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 Planctomycetaceae; Gemmata.
 1 (bases 1 to 574)

REFERENCE
 AUTHORS Jenkins,C., Kedari,V. and Fuerst,J.A.
 TITLE Gene discovery from sequence tags generated using genomic DNA libraries constructed from representatives of the planctomycete division of the Domain Bacteria
 JOURNAL Unpublished (2001)
 COMMENT Contact: Fuerst JA
 Department of Microbiology and Parasitology
 University of Queensland
 Brisbane, QLD 4072, Australia
 Tel: +617 3365 4643
 Fax: +617 3365 4620
 Email: fuerst@biosci.uq.edu.au
 Class: shotgun.

FEATURES
 source
 Location/Qualifiers
 1..574
 /organism="Gemmata obscuriglobus"
 /strain="ACM 2246"
 /db_xref="taxon:114"
 /clone="G139"
 /clone_lib="Gemmata obscuriglobus phagemid library"
 /lab_host="Escherichia coli strain XL1-Blue"
 /note="Vector: pBluescript II SK(-) phagemid; Site 1: BamHI; Site 2: BamHI; Purified genomic DNA from Gemmata obscuriglobus was restricted with Sau3AI to give fragments of 400-3000bp and ligated into the BamHI site of the pBluescript II SK(-) phagemid. The ligated DNA was electroporated into E. coli XL1-Blue."

BASE COUNT 117 a 161 c 163 g 130 t 3 others

ORIGIN

Query Match 47.7%; Score 69.2; DB 17; Length 574;
 Best Local Similarity 90.2%; Pred. No. 9.6e-13;
 Matches 74; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 31 TTGACGCGGCGCGGATGCCCGGCTGACGAGATTCGATTCACCTTATGATA 90
 |||
 DB 408 TTGACGCGGCTACTGTGTTATCCCGGCTGACGAGATTCGATTCACCTTATGATA 467
 |||

QY 91 CCGTGCACCTCGAGGGGGGCC 112
 |||
 DB 468 CCGTGCACCTCGAGGGGGGCC 489
 |||

RESULT 12

CNS06UF5

LOCUS 912 bp DNA linear GSS 06-JUL-2001

DEFINITION T7 end of clone AX0A008E09 of library AX0A from strain CBS 7064 of Pichia farinosa, genomic survey sequence.

ACCESSION ALA15767

VERSION ALA15767.1 GI:12195405

KEYWORDS GSS.

SOURCE Pichia farinosa.

ORGANISM Pichia farinosa
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Saccharomycetaceae; Pichia.

REFERENCE
 AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuvéglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekala,F., Toffano-Nioche,C., Mesolowski-Louvel,M., Wincker,P. and Weissenbach,J.
 TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
 JOURNAL FEMS Lett. 487 (1), 3-12 (2000)
 MEDLINE 20584711
 PUBMED 11152876

REFERENCE
 AUTHORS 2 (bases 1 to 912)
 TITLE de Montigny,J., Spennet,C., Souciet,J., Tekala,F., Dujon,B., Wincker,P., Artiguenave,F. and Potier,S.
 TITLE Genomic exploration of the hemiascomycetous yeasts: 15. Pichia sorbitophila
 JOURNAL FEMS Lett. 487 (1), 87-90 (2000)
 MEDLINE 20584725
 PUBMED 11152890

REFERENCE
 AUTHORS 3 (bases 1 to 912)
 TITLE Direct Submission
 JOURNAL Submitted (07-SEP-2000) Genoscope - Centre National de Séquençage, 2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequelegenoscope.cns.fr - Web: www.genoscope.cns.fr)

COMMENT
 This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES
 source
 Location/Qualifiers
 1..912
 /organism="Pichia farinosa"
 /strain="CBS 7064"
 /db_xref="taxon:4920"
 /clone="AX0A008E09"
 /clone_lib="AX0AA"
 /note="End: T7"

BASE COUNT 298 a 210 c 160 g 240 t 4 others

ORIGIN

Query Match 47.7%; Score 69.2; DB 17; Length 912;
 Best Local Similarity 88.1%; Pred. No. 9.8e-13;
 Matches 74; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 47 TGGATCCCGCGGGCTGACGAGATTCGATTCAGCTTATCGATCCGTCGAGGG 106
 |||
 DB 817 TGGATCCCGCGGGCTGACGAGATTCGATTCAGCTTATCGATCCGTCGAGGG 876
 |||

QY 107 GGGGCTACTACTAATTTGTT 130
 |||
 DB 877 GGGGCTACTACTAATTTGTT 900
 |||

RESULT 13
 BE428068

LOCUS BE428068 162 bp mRNA linear EST 26-JUL-2000
 DEFINITION MTD002.H107990615 ITEC MTD Durum Wheat Root Library Triticum
 turgidum subsp. durum cDNA clone MTD002.H10, mRNA sequence.
 ACCESSION BE428068
 VERSION BE428068.1 GI:9425911
 KEYWORDS EST.
 SOURCE durum wheat.
 ORGANISM Triticum turgidum subsp. durum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
 ; Triticaceae; Triticum.
 1 (bases 1 to 162)
 REFERENCE
 AUTHORS Anderson O.A., Appels R., Bailey P., Blake T., Close T., Cloutier
 S., Dubcovsky J., Feuillet C., Gale M., Graner A., Gustafson P.,
 Herrmann R.G., Holton T., Jacquemin J.M., Jia J., Joudrier P.,
 Langridge P., Izzo G.R., Lin J.J., McGuire P., Ogihara Y.,
 Pecchioli N., Qualset C., Schuch W., Selvaraj G., Shariflou M.,
 Sorrells M., Warburton M. and Wenzel G.
 International Triticaceae EST Cooperative (ITEC): Production of
 International Triticaceae EST Cooperative (ITEC): Production of
 Expressed Sequence Tags for Species of the Triticaceae
 Unpublished (2000)
 CONTACT: Joudrier P
 INRA, Unite de Biochimie et Biologie Molculaire des Cereales
 2, place VIALA, 34060 Montpellier cedex 01 FRANCE
 Tel: 33 4 99 61 23 84
 Fax: 33 4 99 61 23 48
 Email: joudrier@enscm.inra.fr
 International Triticaceae EST Cooperative (ITEC)
 http://wheat.pw.usda.gov/genome.
 FEATURES
 source
 1..162
 /organism="Triticum turgidum subsp. durum"
 /cultivar="Silihana"
 /db_xref="taxon:4567"
 /clone_lib="MTD002.H10"
 /clone_lib="ITEC MTD Durum Wheat Root Library"
 /tissue_type="root"
 /dev_stage="3-day-old seedling, water-stressed"
 /note="Vector: pSPORT1; T7 primers used. See pSPORT1
 polylinker site. 0.3-2.0 kbp average insert size."
 BASE COUNT 28 a 42 c 49 g 43 t
 ORIGIN
 Query Match 47.6%; Score 69; DB 10; Length 162;
 Best Local Similarity 88.2%; Pred. No. 1.1e-12;
 Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 46 GTGATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 105
 |||||||
 DB 24 GTGATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 83
 |||||||
 QY 106 GGGGCGCTACACTAATTTGTT 130
 |||||||
 DB 84 GGGGCGCGGTACCAAGCTTTGTT 108
 |||||||
 RESULT 14
 LOCUS AU234451 390 bp mRNA linear EST 21-SEP-2001
 DEFINITION AU234451 Bovine placenta cDNA Bos taurus cDNA Cln1153 3',
 mRNA sequence.
 ACCESSION AU234451
 VERSION AU234451.1 GI:15719669
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bos.
 1 (bases 1 to 390)
 REFERENCE
 AUTHORS Gohma H., Lejukole H.Y., Taniguchi Y., Yamada T., Akagi S., Yasue
 H. and Sasaki Y.
 Analysis of expressed sequence tags from a cDNA library of bovine

JOURNAL placenta
 COMMENT Unpublished (2001)
 Contact: Takahisa Yamada
 Graduate School of Agriculture
 Kyoto University
 Sakyo-ku, Kitashirakawa, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-6323
 Fax: 81-75-753-6340
 Email: tyamada@kans.kyans.kais.kyoto-u.ac.jp
 This clone was obtained from a 3' end cDNA library.
 FEATURES
 source
 1..390
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="Cln1153"
 /clone_lib="Bovine placenta cDNA"
 /tissue_type="placenta"
 /note="Vector: pUC18 Sma I/BAP"
 BASE COUNT 113 a 77 c 128 t
 ORIGIN
 Query Match 47.6%; Score 69; DB 9; Length 390;
 Best Local Similarity 88.2%; Pred. No. 1.1e-12;
 Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 46 GTGATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 105
 |||||||
 DB 300 GTGATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 359
 |||||||
 QY 106 GGGGCGCTACACTAATTTGTT 130
 |||||||
 DB 360 GGGGCGCGGTACCAAGCTTTGTT 384
 |||||||
 RESULT 15
 LOCUS AU278852/c 400 bp mRNA linear EST 02-JUL-2002
 DEFINITION AU278852 Cloned bovine placenta cDNA Bos taurus cDNA clone
 placental1153 3', mRNA sequence.
 ACCESSION AU278852
 VERSION AU278852.1 GI:21682162
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bos.
 1 (bases 1 to 400)
 REFERENCE
 AUTHORS Oishi M., Yamada T., Goma H., Lejukole H.Y., Taniguchi Y. and
 Sasaki Y.
 EST analysis of cloned bovine fetus and placenta
 Unpublished (2002)
 CONTACT: Masahito Oishi
 Graduate School of Agriculture
 Kyoto University
 Sakyo-ku Kitashirakawa, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-6331
 Fax: 81-75-753-6340
 Email: oishi@kans.kyans.kais.kyoto-u.ac.jp.
 Location/Qualifiers
 1..400
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="placental1153"
 /clone_lib="Cloned bovine placenta cDNA"
 /dev_stage="60 embryonic day"
 /note="Organ: ovary; Vector: pGEM-T Easy; Randomly cloned
 third differential products (DP3) of a Representational
 Differential Analysis (RDA) with bovine corpus luteum as
 tester tissue and skeletal muscle as driver."
 BASE COUNT 133 a 73 c 79 g 115 t
 ORIGIN

	Query Match	Best Local Similarity	Score 69;	DB 9;	Length 400;
	Matches 75;	Conservative	47.6%;	88.2%;	Pred. No. 1.1e-12;
			0;	Mismatches 10;	Indels 0;
					Gaps 0;
QY	46	GGGATCCCGGGGTGGAGGAATTCGATATCACTATCGATCCGTCAGCTCGAGG	105		
DB	91	GGGATCCCGGGGTGGAGGAATTCGATATCACTATCGATCCGTCAGCTCGAGG	32		
QY	106	GGGGCTTAATACTAATTTGTT	130		
DB	31	GGGGCTTAATACTAATTTGTT	7		

Search completed: November 10, 2002, 08:33:09
Job time : 1310 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 04:19:15 ; Search time 171.087 Seconds
(without alignments)
1908.619 Million cell updates/sec

Title: US-08-935-377-6

Perfect score: 145
Sequence: 1 GGCCAAATGTAATACTA.....TTGTTTGTGGCCGCCGCC 145

Scoring table: IDENTITY_NUC
Gap 10.0 , Capex 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SID52/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:*
2: /SID52/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*
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4: /SID52/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:*
5: /SID52/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:*
6: /SID52/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:*
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21: /SID52/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:*
23: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	145	100.0	145	21	AAA15235 Nucleotide sequence
2	145	100.0	145	22	ABA01476 Partial p7.5/ATG0/
3	145	100.0	145	24	AAA01778 Modified p7.5/tk v
4	132	91.0	148	21	AAA15236 Nucleotide sequence
5	132	91.0	148	22	ABA01477 Partial p7.5/ATG1/
6	132	91.0	148	24	AAA01779 Modified p7.5/tk v
7	131	90.3	149	21	AAA15237 Nucleotide sequence
8	131	90.3	149	22	ABA01478 Partial p7.5/ATG2/
9	131	90.3	149	24	AAA01780 Modified p7.5/tk v

10	130	89.7	150	21	AAA15238 Nucleotide sequence
11	130	89.7	150	22	ABA01479 Partial p7.5/ATG3/
12	130	89.7	150	24	AAA01781 Modified p7.5/tk v
13	71.6	49.4	460	23	ABV33323 Human prostate exp
14	71.6	49.4	460	23	ABV33326 Human prostate exp
15	70.8	48.8	508	23	ABV39281 Human prostate exp
16	70.6	48.7	333	23	ABV45519 Human prostate exp
17	70.6	48.7	392	23	ABV38605 Human prostate exp
18	70.6	48.7	455	23	ABV31882 Human prostate exp
19	70.6	48.7	459	23	ABV35787 Human prostate exp
20	70.6	48.7	552	23	ABV44587 Human prostate exp
21	70.6	48.7	552	23	ABV35639 Human prostate exp
22	70.6	48.7	659	23	ABV39144 Human prostate exp
23	70.6	48.7	659	23	ABV45482 Human prostate exp
24	70.6	48.7	659	23	ABV45486 Human prostate exp
25	70.4	48.6	276	23	ABV35118 Human prostate exp
26	70.4	48.6	375	23	ABV44301 Human prostate exp
27	70.4	48.6	5592	24	AAA035631 Plasmid pTV05 full
28	70.2	48.4	5804	24	ABA96439 Plasmid pSV05 SEQ
29	70	48.3	377	23	ABV37034 Human prostate exp
30	70	48.3	400	23	ABV33919 Human prostate exp
31	70	48.3	400	23	ABV42794 Human prostate exp
32	70	48.3	439	23	ABV38640 Human prostate exp
33	70	48.3	567	23	ABV31904 Human prostate exp
34	70	48.3	567	23	ABV40860 Human prostate exp
35	70	48.3	626	23	ABV34271 Human prostate exp
36	70	48.3	630	23	ABV35248 Human prostate exp
37	69.6	48.0	505	23	ABV33645 Human prostate exp
38	69.6	48.0	505	23	ABV42560 Human prostate exp
39	69.4	47.9	411	23	ABV36341 Human prostate exp
40	69.4	47.9	411	23	ABV45372 Human prostate exp
41	69.4	47.9	916	24	AAA45542 E gossypii coding
42	69.4	47.9	13558	22	AA16274 Murine apoptase L1
43	69.2	47.7	437	23	ABV38437 Human prostate exp
44	69	47.6	184	23	ABV35188 Human prostate exp
45	69	47.6	205	23	ABV31861 Human prostate exp

ALIGNMENTS

RESULT 1	
AAA15235	standard; DNA; 145 BP.
ID	AAA15235 standard; DNA; 145 BP.
XX	
AC	AAA15235:
XX	
DT	04-SEP-2000 (first entry)
XX	
DE	Nucleotide sequence of a fragment of the plasmid p7.5/ATG0/tk.
XX	
KW	Vaccinia transfer plasmid; epitope; tumour specific epitope; antigen;
KM	vaccine; tumour regression; cancer; infection; ss.
XX	
OS	Synthetic.
XX	
PN	WO200028016-A1.
XX	
PD	18-MAY-2000.
XX	
PF	10-NOV-1998; 98WO-US24029.
XX	
PR	10-NOV-1998; 98WO-US24029.
XX	
PA	(UYRP) UNIV ROCHESTER.
XX	
PI	Zauderer M;
XX	
DR	WPI; 2000-376533/32.
XX	
PT	Novel method of identifying target epitopes or antigens specific for
PT	human tumors, cancers and infected cells involving screening expression
PT	library products of a cell expressing the target epitope

XX PS Disclosure; Fig 2; 132pp; English.
 CC CC The present sequence represents a fragment of a vaccinia transfer
 CC CC plasmid, which is used in the course of the invention. The
 CC CC specification describes a method for identifying a target epitope.
 CC CC The method comprises screening the products of an expression library
 CC CC from a cell expressing the target epitope with cytotoxic T cells
 CC CC generated against the cell to identify DNA clones expressing the target
 CC CC epitope. The method may also comprise providing a cytotoxic T cell
 CC CC specific for a gene product differentially expressed by a cell and
 CC CC measuring the cross-reactivity of the cytotoxic T cell. The methods are
 CC CC useful for identifying tumour specific target epitopes and antigens which
 CC CC are useful in immunogenic compositions or vaccines to induce the
 CC CC regression of tumors, cancers or infections in mammals. The genes
 CC CC expressed in a panel of tumour cells that are derived from single
 CC CC immortalised, non-tumorigenic cell line are used to generate HLA
 CC CC restricted cytotoxic T cells which are evaluated for activity against
 CC CC tumour cells. The method is useful to identify potential antigens
 CC CC expressed not only by the pathogen but also by the host cells whose gene
 CC CC expression is altered as a result of infection. The differential gene
 CC CC expression strategies can be applied to identify immunogenic molecules
 CC CC of cells infected with virus, fungus or mycobacterium.
 XX SQ Sequence 145 BP; 34 A; 37 C; 38 G; 36 T; 0 other;
 Query Match 100.0%; Score 145; DB 21; Length 145;
 Best Local Similarity 100.0%; Pred. No. 2,1e-40;
 Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGCCTAAATTTGAAAACCTAGATCTATTATTGACGCGCGCCGCTGATCCCCGGGC 60
 Db 1 GGCCTAAATTTGAAAACCTAGATCTATTATTGACGCGCGCCGCTGATCCCCGGGC 60
 QY 61 TGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACGCGGGGGGCGCTACTAAC 120
 Db 61 TGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACGCGGGGGGCGCTACTAAC 120
 QY 121 TAATTTGTTTTGTGGGCGCGCC 145
 Db 121 TAATTTGTTTTGTGGGCGCGCC 145

RESULT 2
 ABA01476
 ID ABA01476 standard; DNA; 145 BP.
 AC ABA01476;
 XX
 DT 04-FEB-2002 (first entry)
 DE Partial p7.5/ATG0/tk sequence.
 DE
 XX Cell death; toxic gene; tumour suppressor; ds.
 KM
 XX Synthetic.
 OS
 PN W0200172995-A2.
 PD 04-OCT-2001.
 PF 28-MAR-2001; 2001WO-US09953.
 PR 28-MAR-2001; 2000US-0192586.
 PR 10-MAY-2000; 2000US-0203343.
 PR 23-JAN-2001; 2001US-0263226.
 PR 27-FEB-2001; 2001US-0271426.
 XX
 PA (UYRP) UNIV ROCHESTER.
 XX
 PI Zauderer M, Smith ES;
 XX
 DR WPI; 2001;570897/64.

XX PS Selecting target polynucleotides, particularly toxic genes, involves
 PT introducing a library of insert polynucleotides into a host cell
 PT population, where the target polynucleotide promotes cell death -
 XX
 XX PS Disclosure; Fig 8; 359pp; English.
 CC CC The present invention relates to a method for selecting a target
 CC CC polynucleotide. The method comprises introducing into a host cell
 CC CC population a library of insert polynucleotides, where expression of the
 CC CC target polynucleotide directly or indirectly promotes host cell death.
 CC CC The cells are cultured and the insert polynucleotides are collected from
 CC CC the cells which die. The method is useful for selecting target
 CC CC polynucleotides, particularly polynucleotides which alter cell phenotypes
 CC CC of induce or inhibit cell death. The method can be used to isolate toxic
 CC CC genes such as tumour suppressors. The present sequence was used to
 CC CC illustrate the method of the present invention.
 XX SQ Sequence 145 BP; 34 A; 37 C; 38 G; 36 T; 0 other;
 Query Match 100.0%; Score 145; DB 22; Length 145;
 Best Local Similarity 100.0%; Pred. No. 2,1e-40;
 Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGCCTAAATTTGAAAACCTAGATCTATTATTGACGCGCGCCGCTGATCCCCGGGC 60
 Db 1 GGCCTAAATTTGAAAACCTAGATCTATTATTGACGCGCGCCGCTGATCCCCGGGC 60
 QY 61 TGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACGCGGGGGGCGCTACTAAC 120
 Db 61 TGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACGCGGGGGGCGCTACTAAC 120
 QY 121 TAATTTGTTTTGTGGGCGCGCC 145
 Db 121 TAATTTGTTTTGTGGGCGCGCC 145

RESULT 3
 AAD31778
 ID AAD31778 standard; DNA; 145 BP.
 AC AAD31778;
 XX
 DT 18-JUN-2002 (first entry)
 DE Modified p7.5/tk vector, p7.5/ATG0/tk.
 DE
 XX Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;
 KM vaccine; immune response; cytostatic; p7.5/tk vector; thymidine kinase;
 KM p7.5/ATG0/tk vector; ds.
 XX
 OS Vaccinia virus.
 OS Synthetic.
 FH
 FT Key location/Qualifiers
 FT mISC_signal 113..115
 FT /tag= a
 FT /note= "translation stop codon"
 FT 117..119
 FT /tag= b
 FT /note= "translation stop codon"
 FT 121..123
 FT /tag= c
 FT /note= "translation stop codon"
 FT 129..135
 FT /tag= d
 FT /note= "transcription stop signal"
 XX
 XX US2002018785-A1.
 XX
 PD 14-FEB-2002.
 XX
 PF 02-APR-2001; 2001US-0822250.


```
XX 22-SEP-1997; 970S-0935377.
XX (UYRP ) UNIV ROCHESTER.
XX Zauderer M;
XX WPI; 2002-239252/29.
XX
XX Representational Difference Analysis method for identification of
XX antigens recognized by cytotoxic T cells and specific for human tumors,
XX comprises improved selection of genes encoding target antigens -
XX
XX Example 1; Fig 2; 54pp; English.
XX
XX The present invention relates to novel methods for the identification
XX of antigens recognised by cytotoxic T cells (CTLs) and specific for
XX human tumours, cancers and infected cells. The method involves screening
XX the products of an expression library generated from DNA/RNA of a cell
XX expressing a target epitope with cytotoxic T cells generated against
XX the cell to identify DNA clones expressing target epitope or providing
XX cytotoxic T cells specific for a gene product differentially expressed
XX by a cell and measuring the cross-reactivity of the cytotoxic T cells
XX for cells expressing a target epitope in which the target epitope is
XX identified as a gene product inducing cytotoxic T cells. The method is
XX useful for identifying a target epitope or antigen specific for a tumour
XX cell. The target epitope is also useful for identifying target antigens
XX in other target cells against which it is desirable to induce cell-
XX mediated immunity. The antigen identified by the method is useful
XX in immunogenic compositions and vaccine preparations to induce the
XX regression of tumours, cancers and infections in mammals. The invention
XX also relates to vaccinia viral vectors which are useful for treating
XX tumour-bearing mammals, including humans to generate immune response
XX against the tumour cells. They are also useful for immunising or
XX vaccinating tumour-free subjects to prevent tumour formation. The
XX present sequence is modified p7.5/tk (thymidine kinase) vector.
XX p7.5/ATG0/tk. This vector comprises a vaccinia virus 7.5K promoter and
XX a modified tk DNA fragment. This vector is used in the exemplification
XX of the invention.
XX
XX Sequence 145 BP; 34 A; 37 C; 38 G; 36 T; 0 other;
XX
XX Query Match 100.0%; Score 145; DB 24; Length 145;
XX Best Local Similarity 100.0%; Pred. No. 2.1e-40;
XX Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GGCCTAAATTTGAAAACTAGATCTATTATTCACGCGCGCGCGTGCATCCCGCGGC 60
XX |
XX |
XX |
XX 1 GGCCTAAATTTGAAAACTAGATCTATTATTCACGCGCGCGCGTGCATCCCGCGGC 60
XX
XX QY 61 TGCAGGAATTCGATATCACTATGATACCGTCGACCTCGAGGGGGGCGCTTAAC 120
XX |
XX |
XX |
XX 61 TGCAGGAATTCGATATCACTATGATACCGTCGACCTCGAGGGGGGCGCTTAAC 120
XX
XX QY 121 TAATTTGTTTGTGGCGCGCGC 145
XX |
XX |
XX |
XX 121 TAATTTGTTTGTGGCGCGCGC 145
XX
XX Db 121 TAATTTGTTTGTGGCGCGCGC 145
XX
XX
XX RESULT 4
XX AAA15236
XX ID AAA15236 standard; DNA; 148 BP.
XX
XX AC AAA15236;
XX
XX 04-SEP-2000 (first entry)
XX
XX Nucleotide sequence of a fragment of the plasmid p7.5/ATG1/tk.
XX
XX Vaccinia transfer plasmid; epitope; tumour specific epitope; antigen;
XX vaccine; tumour regression; cancer; infection; ss.
XX
XX OS Synthetic.
```

```
XX WO200028016-A1.
XX
XX 18-MAY-2000.
XX
XX 10-NOV-1998; 98WO-US24029.
XX
XX 10-NOV-1998; 98WO-US24029;
XX
XX (UYRP ) UNIV ROCHESTER.
XX Zauderer M;
XX WPI; 2000-376533/32.
XX
XX Novel method of identifying target epitopes or antigens specific for
XX human tumors, cancers and infected cells involving screening expression
XX library products of a cell expressing the target epitope -
XX
XX Disclosure; Fig 2; 132pp; English.
XX
XX The present sequence represents a fragment of a vaccinia transfer
XX plasmid, which is used in the course of the invention. The
XX specification describes a method for identifying a target epitope.
XX The method comprises screening the products of an expression library
XX from a cell expressing the target epitope with cytotoxic T cells
XX generated against the cell to identify DNA clones expressing the target
XX epitope. The method may also comprise providing a cytotoxic T cell
XX specific for a gene product differentially expressed by a cell and
XX measuring the cross-reactivity of the cytotoxic T cell. The methods are
XX useful for identifying tumour specific target epitopes and antigens which
XX are useful in immunogenic compositions or vaccines to induce the
XX regression of tumours, cancers or infections in mammals. The genes
XX expressed in a panel of tumour cells that are derived from single
XX immortalised, non-tumourigenic cell line are used to generate HLA
XX restricted cytotoxic T cells which are evaluated for activity against
XX tumour cells. The method is useful to identify potential antigens
XX expressed not only by the pathogen but also by the host cells whose gene
XX expression is altered as a result of infection. The differential gene
XX expression strategies can be applied to identify immunogenic molecules
XX of cells infected with virus, fungus or mycobacterium.
XX
XX Sequence 148 BP; 35 A; 37 C; 39 G; 37 T; 0 other;
XX
XX Query Match 91.0%; Score 132; DB 21; Length 148;
XX Best Local Similarity 98.0%; Pred. No. 6.6e-36;
XX Matches 145; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
XX
XX QY 1 GGCCTAAATTTGAAAACTAGATCTATTATTCACGCGCGCGCGTGCATCCCGCG 57
XX |
XX |
XX |
XX 1 GGCCTAAATTTGAAAACTAGATCTATTATTCACGCGCGCGCGTGCATCCCGCG 60
XX
XX Db 58 GCGTCGAGGAATTCGATATCAAGCTTATGATACCGTCGACCTCGAGGGGGGCGCTTA 117
XX |
XX |
XX |
XX 61 GCGTCGAGGAATTCGATATCAAGCTTATGATACCGTCGACCTCGAGGGGGGCGCTTA 120
XX
XX QY 118 AACTAATTTTGTGTTGTGGCGCGCGC 145
XX |
XX |
XX |
XX 121 AACTAATTTTGTGTTGTGGCGCGCGC 148
XX
XX Db 121 AACTAATTTTGTGTTGTGGCGCGCGC 148
XX
XX
XX RESULT 5
XX ABA01477
XX ID ABA01477 standard; DNA; 148 BP.
XX
XX AC ABA01477;
XX
XX 04-FEB-2002 (first entry)
XX
XX Partial p7.5/ATG1/tk sequence.
XX
XX Cell death; toxic gene; tumour suppressor; ds.
XX
```

OS	Synthetic.
XX	
PN	WO200172995-A2.
PD	
PD	04-OCT-2001.
XX	
PF	28-MAR-2001; 2001WO-US09953.
XX	
PR	28-MAR-2000; 2000US-0192586.
PR	10-MAY-2000; 2000US-0203343.
PR	23-JAN-2001; 2001US-0263228.
PR	27-FEB-2001; 2001US-0271426.
PA	(UYRP) UNIV ROCHESTER.
XX	
P1	Zauderer M., Smith ES;
XX	
DR	WPI: 2001-570897/64.
XX	
PT	Selecting target polynucleotides, particularly toxic genes, involves
PT	introducing a library of insert polynucleotides into a host cell
PT	population, where the target polynucleotide promotes cell death -
XX	
PS	Disclosure: Fig 8; 35pp; English.
XX	
CC	The present invention relates to a method for selecting a target
CC	polynucleotide. The method comprises introducing into a host cell
CC	a population a library of insert polynucleotides, where expression of the
CC	target polynucleotide directly or indirectly promotes host cell death.
CC	The cells are cultured and the insert polynucleotides are collected from
CC	the cells which die. The method is useful for selecting target
CC	polynucleotides, particularly polynucleotides which alter cell phenotypes
CC	of induce or inhibit cell death. The method can be used to isolate toxic
CC	genes such as tumour suppressors. The present sequence was used to
CC	illustrate the method of the present invention.
XX	
SQ	Sequence 148 BP; 35 A; 37 C; 39 G; 37 T; 0 other;
	Query Match 91.0%; Score 132; DB 22; Length 148;
	Best Local Similarity 98.0%; Pred. No. 6,6e-36;
	Matches 145; Conservative 0; Mismatches 0; Indels 3; Gaps 1.
OY	1 GGCACAAAATTAAGAAACAGATCTATTATTCACGCGGCCGCC---GTGGATCCCCG 57
DB	1 GCCCAAAAAATTAAGAAACAGATCTATTATTCACGCGGCCGCCCATGTGCAATCCC 60
OY	58 GGCTCAGAGAATTCGATATCAAGCTTATGATACCGTCGACTCGAAGGGGGCCCTAACT 117
DB	61 GGCCTCAGAGAATTCGATATCAAGCTTATGATACCGTCGACTCGAAGGGGGCCCTAACT 120
OY	118 AACATAATTTTGTTTTGTTGGGCCGCCGCC 145
DB	121 AACATAATTTTGTTTTGTTGGGCCGCCGCC 148
	RESULT 6
AAD31779	
ID	AAD31779 standard: DNA; 148 BP.
XX	
AC	AAD31779;
XX	
DT	18-JUN-2002 (first entry)
XX	
DE	Modified p7.5/tk vector. p7.5/ATG1/tk.
XX	
KW	Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;
KW	vaccine; immune response; cytostatic; p7.5/tk vector; thymidine kinase;
KW	p7.5/ATG1/tk vector; ds.
XX	
OS	Vaccinia virus.
XX	
OS	Synthetic.
XX	
FH	Key , Location/Qualifiers

```

FT      misc_signal      46...48      /*tag= a
FT      /note= "Translation start codon"
FT      misc_signal      116...118      /*tag= b
FT      /note= "Translation stop codon"
FT      misc_signal      120...122      /*tag= c
FT      /note= "Translation stop codon"
FT      misc_signal      124...126      /*tag= d
FT      /note= "Translation stop codon"
FT      misc_signal      132...138      /*tag= e
FT      /note= "Transcription stop signal"
XX
XX      US2002018785-A1.
XX
XX      14-FEB-2002.
XX
XX      02-APR-2001; 2001US-0822250.
XX
XX      22-SEP-1997; 97US-0935377.
XX
XX      (UYRP ) UNIV ROCHESTER.
XX
XX      Zauderer M;
XX
XX      WPI; 2002-239252/29.
XX
XX      Representative Difference Analysis method for identification of
XX      antigens recognized by cytotoxic T cells and specific for human tumors,
XX      comprises improved selection of genes encoding target antigens
XX
XX      Example 1; Fig 2; 54pp; English.
XX
XX      The present invention relates to novel methods for the identification
XX      of antigens recognised by cytotoxic T cells (CTRs) and specific for
XX      human tumours, cancers and infected cells. The method involves screening
XX      the products of an expression library generated from DNA/RNA of a cell
XX      expressing a target epitope with cytotoxic T cells generated against
XX      the cell to identify DNA clones expressing target epitope or providing
XX      cytotoxic T cells specific for a gene product differentially expressed
XX      by a cell and measuring the cross-reactivity of the cytotoxic T cells
XX      for cells expressing a target epitope in which the target epitope is
XX      identified as a gene product inducing cytotoxic T cells. The method is
XX      useful for identifying a target epitope or antigen specific for a tumour
XX      cell. The target epitope is also useful for identifying target antigens
XX      in other target cells against which it is desirable to induce cell-
XX      mediated immunity. The antigen identified by the method is useful
XX      in immunogenic compositions and vaccine preparations to induce the
XX      regression of tumours, cancers and infections in mammals. The invention
XX      also relates to vaccinia viral vectors which are useful for treating
XX      tumour-bearing mammals, including humans to generate immune response
XX      against the tumour cells. They are also useful for immunising or
XX      vaccinating tumour-free subjects to prevent tumour formation. The
XX      present sequence is modified p7.5/tk (thymidine kinase) vector,
XX      p7.5/ANG1/tk. This vector comprises a vaccinia virus 7.5k promoter and
XX      a modified tk DNA fragment. This vector is used in the exemplification
XX      of the invention.
XX
XX      Sequence 148 BP; 35 A; 37 C; 39 G; 37 T; 0 other;
XX
XX      Query Match      91.0%; Score 132; DB 24; Length 148;
XX      Best Local Similarity 98.0%; Pred. No. 6.6e-36;
XX      Matches 145; Conservative 0; Mismatches 0; Indels 3; Gaps 1
XX
XX      1 GGCACAAAATGTGAAGCTTATGATACCGTCGACCTCGAGGGGGGCGCTAAGC 57
XX      |||||||
XX      Db 1 GGCACAAAATGTGAAGCTTATGATACCGTCGACCGGCGCCATGGTGTATCCCG 60
XX      |||||||
XX      58 GCGTCGAGGAATTCGATATCAAGCTTATGATACCGTCGACCTCGAGGGGGGCGCTAAGC 117
XX      |||||||

```

Db 61 GCGTCAGGAATTCGATATACGCTTATCGATACCGTCGACCTGAGGGGGCCCTAACT 120
QY 118 AACTAATTTGTTTGTGGGCGCCGCC 145
| | | | |
Db 121 AACTAATTTGTTTGTGGGCGCCGCC 148

RESULT 7
AAAI5237
ID AAAI5237 standard; DNA; 149 BP.
XX

AC AAAI5237;
XX

DT 04-SEP-2000 (first entry)
XX

DE Nucleotide sequence of a fragment of the plasmid p7.5/ATG2/tk.
XX

KM Vaccinia transfer plasmid; epitope; tumour specific epitope; antigen;
XX vaccine; tumour regression; cancer; infection; ss.
XX

OS Synthetic.
XX

PN WO200028016-A1.
XX

PD 18-MAY-2000.
XX

PF 10-NOV-1998; 98WO-US24029.
XX

PR 10-NOV-1998; 98WO-US24029.
XX

PA (UYRP) UNIV ROCHESTER.
XX

P1 Zauderer M;
XX

DR WPI: 2000-376533/32.
XX

PT Novel method of identifying target epitopes or antigens specific for
PT human tumors, cancers and infected cells involving screening expression
PT library products of a cell expressing the target epitope -
XX
PS Disclosure; Fig 2; 132pp; English.

CC The present sequence represents a fragment of a vaccinia transfer
CC plasmid, which is used in the course of the invention. The
CC specification describes a method for identifying a target epitope.
CC The method comprises screening the products of an expression library
CC from a cell expressing the target epitope with cytotoxic T cells
CC generated against the cell to identify DNA clones expressing the target
CC epitope. The method may also comprise providing a cytotoxic T cell
CC specific for a gene product differentially expressed by a cell and
CC measuring the cross-reactivity of the cytotoxic T cell. The methods are
CC useful for identifying tumour specific target epitopes and antigens which
CC are useful in immunogenic compositions or vaccines to induce the
CC regression of tumors, cancers or infections in mammals. The genes
CC expressed in a panel of tumour cells that are derived from single
CC immortalised, non-tumorigenic cell line are used to generate HLA
CC restricted cytotoxic T cells which are evaluated for activity against
CC tumour cells. The method is useful to identify potential antigens
CC expressed not only by the pathogen but also by the host cells whose gene
CC expression is altered as a result of infection. The differential gene
CC expression strategies can be applied to identify immunogenic molecules
CC of cells infected with virus, fungus or mycobacterium.
XX
SQ Sequence 149 BP; 36 A; 37 C; 39 G; 37 T; 0 other;

Query Match 90.3%; Score 131; DB 21; Length 149;
Best Local Similarity 97.3%; Pred. No. 1.5e-35;

Matches 145; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 GGGCAAAAATTTGAAAACGATCTATTATTTGACGCGCGCCGCC---CTGATCCCCC 56
| | | | |
Db 1 GGGCAAAAATTTGAAAACGATCTATTATTTGACGCGCGCGCCGCGCATGATGATCCCCC 60

QY 57 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTGAGGGGGCCCTAAC 116
| | | | |
Db 61 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTGAGGGGGCCCTAAC 120
QY 117 TAACATAATTTGTTTGTGGGCGCCGCC 145
| | | | |
Db 121 TAACATAATTTGTTTGTGGGCGCCGCC 149

RESULT 8
ABA01478
ID ABA01478 standard; DNA; 149 BP.
XX

AC ABA01478;
XX

DT 04-FEB-2002 (first entry)
XX

DE Partial p7.5/ATG2/tk sequence.
XX

KM Cell death; toxic gene; tumour suppressor; ds.
XX

OS Synthetic.
XX

PN WO200172995-A2.
XX

PD 04-OCT-2001.
XX

PF 28-MAR-2001; 2001WO-US09953.
XX

PR 28-MAR-2000; 2000US-0192586.
XX

PR 10-MAY-2000; 2000US-0203343.
XX

PR 23-JAN-2001; 2001US-0263226.
XX

PR 27-FEB-2001; 2001US-0271426.
XX

PA (UYRP) UNIV ROCHESTER.
XX

P1 Zauderer M, Smith BS;
XX

DR WPI: 2001-570897/64.
XX

PT Selecting target polynucleotides, particularly toxic genes, involves
PT introducing a library of insert polynucleotides into a host cell -
PT population, where the target polynucleotide promotes cell death -
XX
PS Disclosure; Fig 8; 359pp; English.

CC The present invention relates to a method for selecting a target
CC polynucleotide. The method comprises introducing into a host cell
CC population a library of insert polynucleotides, where expression of the
CC target polynucleotide directly or indirectly promotes host cell death.
CC The cells are cultured and the insert polynucleotides are collected from
CC the cells which die. The method is useful for selecting target
CC polynucleotides, particularly polynucleotides which alter cell phenotypes
CC of induce or inhibit cell death. The method can be used to isolate toxic
CC genes such as tumour suppressors. The present invention was used to
CC illustrate the method of the present invention.
XX
SQ Sequence 149 BP; 36 A; 37 C; 39 G; 37 T; 0 other;

Query Match 90.3%; Score 131; DB 22; Length 149;
Best Local Similarity 97.3%; Pred. No. 1.5e-35;

Matches 145; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 GGGCAAAAATTTGAAAACGATCTATTATTTGACGCGCGCCGCC---GTGATCCCCC 56
| | | | |
Db 1 GGGCAAAAATTTGAAAACGATCTATTATTTGACGCGCGCGCCGCGCATGATGATCCCCC 60

QY 57 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTGAGGGGGCCCTAAC 116
| | | | |
Db 61 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTGAGGGGGCCCTAAC 120

QY 117 TAACATAATTTGTTTGTGGGCGCCGCC 145
| | | | |

Db 121 TAACTAATTTGTTTGTGGGCCGCC 149
RESULT 9
AAD31780
ID AAD31780 standard; DNA: 149 BP.
XX
AC AAD31780;
XX
DT 18-JUN-2002 (first entry)
XX
DE Modified p7.5/tk vector, p7.5/ATG2/tk.
XX
XX Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;
KW vaccine; immune response; cytostatic; p7.5/tk vector; thymidine kinase;
KM p7.5/ATG2/tk vector; ds.
XX
OS Vaccinia virus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_signal 46..48
FT /*tag= a
FT /note= "translation start codon"
FT 117..119
FT /*tag= b
FT /note= "translation stop codon"
FT 121..123
FT /*tag= c
FT /note= "translation stop codon"
FT 125..127
FT /*tag= d
FT /note= "translation stop codon"
FT 133..139
FT /*tag= e
FT /note= "transcription stop signal"
XX
PN US2002018785-A1.
XX
PD 14-FEB-2002.
XX
PF 02-APR-2001; 2001US-0822250.
XX
PR 22-SEP-1997; 97US-0935377.
XX
PA (UYRP) UNIV ROCHESTER.
XX
PI Zauderer M;
XX
DR WPI; 2002-239252/29.
XX
XX
PT Representational Difference Analysis method for identification of
PT antigens recognized by cytotoxic T cells and specific for human tumors,
PT comprises improved selection of genes encoding target antigens -
XX
XX Example 1; Fig 2; 54pp; English.
XX
XX The present invention relates to novel methods for the identification
XX of antigens recognised by cytotoxic T cells (CTLs) and specific for
XX human tumours, cancers and infected cells. The method involves screening
XX the products of an expression library generated from DNA/RNA of a cell
XX expressing a target epitope with cytotoxic T cells generated against
XX the cell to identify DNA clones expressing target epitope or providing
XX cytotoxic T cells specific for a gene product differentially expressed
XX by a cell and measuring the cross-reactivity of the cytotoxic T cells
XX for cells expressing a target epitope in which the target epitope is
XX identified as a gene product inducing cytotoxic T cells. The method is
XX useful for identifying a target epitope or antigen specific for a tumour
XX cell. The target epitope is also useful for identifying target antigens
XX in other target cells against which it is desirable to induce cell-
XX mediated immunity. The antigen identified by the method is useful
XX in immunogenic compositions and vaccine preparations to induce the
XX regression of tumours, cancers and infections in mammals. The invention

CC also relates to vaccinia viral vectors which are useful for treating
CC tumour-bearing mammals, including humans to generate immune response
CC against the tumour cells. They are also useful for immunising or
CC vaccinating tumour-free subjects to prevent tumour formation. The
CC present sequence is modified p7.5/tk (thymidine kinase) vector,
CC p7.5/ATG2/tk. This vector comprises a vaccinia virus 7.5K promoter and
CC a modified tk DNA fragment. This vector is used in the exemplification
CC of the invention.
XX
SQ Sequence 149 BP; 36 A; 37 C; 39 G; 37 T; 0 other;
XX
Query Match 90.3%; Score 131; DB 24; Length 149;
Best Local Similarity 97.3%; Pred. No. 1.5e-35;
Matches 145; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 1 GGGCAAAATTTGAAAACAGATCTATTATGACGGCGGCCGCGCC---GTGGATCCCC 56
DB 1 GGGCAAAATTTGAAAACAGATCTATTATGACGGCGGCCGCGCCATGATGATCCCC 60
QY 57 GGGCTGCAGGAATGCAATGCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCTTAAC 116
DB 61 GGGCTGCAGGAATGCAATGCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCTTAAC 120
QY 117 TAACTAATTTGTTTGTGGGCCGCC 145
DB 121 TAACTAATTTGTTTGTGGGCCGCC 149
XX
RESULT 10
AAAI5238
ID AAI5238 standard; DNA: 150 BP.
XX
AC AAI5238;
XX
DT 04-SEP-2000 (first entry)
XX
XX Nucleotide sequence of a fragment of the plasmid p7.5/ATG3/tk.
DE
XX
KW Vaccinia transfer plasmid; epitope; tumour specific epitope; antigen;
KW vaccine; tumour regression; cancer; infection; ss.
XX
OS Synthetic.
XX
PN WO200028016-A1.
XX
PD 18-MAY-2000.
XX
PF 10-NOV-1998; 98WO-US24029.
XX
PR 10-NOV-1998; 98WO-US24029.
XX
PA (UYRP) UNIV ROCHESTER.
XX
PI Zauderer M;
XX
DR WPI; 2000-376533/32.
XX
XX
PT Novel method of identifying target epitopes or antigens specific for
PT human tumors, cancers and infected cells involving screening expression
PT library products of a cell expressing the target epitope -
XX
XX Disclosure; Fig 2; 132pp; English.
XX
XX The present sequence represents a fragment of a vaccinia transfer
XX plasmid, which is used in the course of the invention. The
XX specification describes a method for identifying a target epitope.
XX The method comprises screening the products of an expression library
XX from a cell expressing the target epitope with cytotoxic T cells
XX generated against the cell to identify DNA clones expressing the target
XX epitope. The method may also comprise providing a cytotoxic T cell
XX specific for a gene product differentially expressed by a cell and
XX measuring the cross-reactivity of the cytotoxic T cell. The methods are
XX useful for identifying tumour specific target epitopes and antigens which

PT antigens recognized by cytotoxic T cells and specific for human tumors,
PT comprises improved selection of genes encoding target antigens -
XX
XX
PS Example 1; Fig 2; 54pp; English.

XX The present invention relates to novel methods for the identification
CC of antigens recognised by cytotoxic T cells (CTLs) and specific for
CC human tumours, cancers and infected cells. The method involves screening
CC the products of an expression library generated from DNA/RNA of a cell
CC expressing a target epitope with cytotoxic T cells generated against
CC the cell to identify DNA clones expressing target epitope or providing
CC cytotoxic T cells specific for a gene product differentially expressed
CC by a cell and measuring the cross-reactivity of the cytotoxic T cells
CC for cells expressing a target epitope in which the target epitope is
CC identified as a gene product inducing cytotoxic T cells. The method is
CC useful for identifying a target epitope or antigen specific for a tumour
CC cell. The target epitope is also useful for identifying target antigens
CC in other target cells against which it is desirable to induce cell-
CC mediated immunity. The antigen identified by the method is useful
CC in immunogenic compositions and vaccine preparations to induce the
CC regression of tumours, cancers and infections in mammals. The invention
CC also relates to vaccinia viral vectors which are useful for treating
CC tumour-bearing mammals, including humans to generate immune response
CC against the tumour cells. They are also useful for immunising or
CC vaccinating tumour-free subjects to prevent tumour formation. The
CC present sequence is modified p7.5/tk (thymidine kinase) vector.
CC p7.5/TK3/tk. This vector comprises a vaccinia virus 7.5K promoter and
CC a modified tk DNA fragment. This vector is used in the exemplification
CC of the invention.

XX Sequence 150 BP; 36 A; 38 C; 39 G; 37 T; 0 other;

XX
XX Query Match 89.7%; Score 130; DB 24; Length 150;
Best Local Similarity 96.7%; Pred. No. 3.3e-35;
Matches 145; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 GGCCTAAATTTGAAATAGATCTATTATTCACGCGGCCGCGC-----CGTGGATCCCC 55
DB 1 GGCCTAAATTTGAAATAGATCTATTATTCACGCGGCCGCGCCTGATGCC 60
QY 56 CGGGCTGAGGAATTCGATCAGCTATGATACCGTGCACCTCGAGGGGGGCGCTAA 115
DB 61 CGGGCTGAGGAATTCGATCAGCTATGATACCGTGCACCTCGAGGGGGGCGCTAA 120
QY 116 CTAACATAATTTGTTTGTGGGCGCGCC 145
DB 121 CTAACATAATTTGTTTGTGGGCGCGCC 150

RESULT 13
ABV33323
ID ABV33323 standard; cDNA; 460 BP.
XX
AC ABV33323;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 33314.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 18-JUL-2000; 2000US-211314P.

PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
XX

PS Claim 1; Page 7060-7061; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

SQ Sequence 460 BP; 118 A; 119 C; 114 G; 109 T; 0 other;

XX
XX Query Match 49.4%; Score 71.6; DB 23; Length 460;
Best Local Similarity 89.5%; Pred. No. 7.7e-15;
Matches 77; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 46 GTGATCCCCCGGGCGTGCAGGAATTCGATCAGCTTACCGTCGACCTCGAGG 105
DB 355 GTGATCCCCCGGGCGTGCAGGAATTCGATCAGCTTACCGTCGACCTCGAGG 414

QY 106 GGGGGCCTAAGTAATTTGTTT 131
DB 415 GGGGGCCCGGTACCCAGCTTGTTT 440

RESULT 14
ABV42246
ID ABV42246 standard; cDNA; 460 BP.
XX
AC ABV42246;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 42237.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.

PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI: 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 8465; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 460 BP; 118 A; 119 C; 114 G; 109 T; 0 other;
XX
Query Match 49.4%; Score 71.6; DB 23; Length 460;
Best Local Similarity 89.5%; Pred. No. 7.7e-15;
Matches 77; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX
QY 46 GTGATCCCGGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCTGACCTGAGG 105
DB 355 GTGATCCCGGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCTGACCTGAGG 414
QY 106 GGGGGCTCACTAAGTAATTTGTTT 131
DB 415 GGGGGCCCGGTAACCAAGCTTTGTTT 440
XX
RESULT 15
ABV39281
ID ABV39281 standard; cDNA: 508 BP.
XX
AC ABV39281;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 39272.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI: 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 7972; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 508 BP; 140 A; 115 C; 125 G; 128 T; 0 other;
XX
Query Match 48.8%; Score 70.8; DB 23; Length 508;
Best Local Similarity 82.7%; Pred. No. 1.5e-14;
Matches 81; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
XX
QY 33 GCACGGGGGCGCGTGCAGAAATTCGATATCAAGCTTATCGATACCTGATAC 92
DB 207 GCAGCGCTCGAAGTGTATCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATAC 266
QY 93 GTGCACCTCGAGGGGGCTCACTAAGTAATTTGTTT 130
DB 267 GTGCACCTCGAGGGGGCGCGTGCAGAAATTCGATATCAAGCTTATCGATAC 304

Search completed: November 10, 2002, 05:58:27
Job time : 173.087 secs


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; APPLICANT: University of Rochester
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
; TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells
; FILE REFERENCE: 1821.0070004
; CURRENT APPLICATION NUMBER: US/09/987,456
; PRIOR APPLICATION NUMBER: 2001-11-14
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/262,067
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/298,087
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/249,268
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 145
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p 7.5/ATG0/tk promoter
US-09-987-456-2

Query Match
Best Local Similarity 100.0%; Score 145; DB 10; Length 145;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 GGCCTAAATTTGAAAACATGATCTATTATTGACAGCGCGCCGCTGATCCCCGGGC 60
Db 1 GGCCTAAATTTGAAAACATGATCTATTATTGACAGCGCGCCGCTGATCCCCGGGC 60
Oy 61 TGCAGGAATTCGATATCAAGCTTATCGATACCGTGCAGGCGGGGGGCGCTAACTAAC 120
Db 61 TGCAGGAATTCGATATCAAGCTTATCGATACCGTGCAGGCGGGGGGCGCTAACTAAC 120
Oy 121 TAATTTGTTTTGTGTGGCCGCGCC 145
Db 121 TAATTTGTTTTGTGTGGCCGCGCC 145
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RESULT 3
US-09-822-250-7
; Sequence 7, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
; CURRENT APPLICATION NUMBER: US/09/822,250
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 148
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-822-250-7
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Query Match
Best Local Similarity 91.0%; Score 132; DB 10; Length 148;
Matches 145; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
Oy 1 GGCCTAAATTTGAAAACATGATCTATTATTGACAGCGCGCCGCTGATCCCCGG 57
Db 1 GGCCTAAATTTGAAAACATGATCTATTATTGACAGCGCGCCGCTGATCCCCGG 60
Oy 58 GGCCTGAGGAATTCGATATCAAGCTTATCGATACCGTGCAGGCGGGGGCGCTAACT 117
```

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Db 61 GGCCTGAGGAATTCGATATCAAGCTTATCGATACCGTGCAGGCGGGGGCGCTAACT 120
Oy 118 AACTAATTTGTTTTGTGTGGCCGCGCC 145
Db 121 AACTAATTTGTTTTGTGTGGCCGCGCC 148
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```
RESULT 4
US-09-987-456-3
; Sequence 3, Application US/09987456
; Patent No. US20020123057A1
; GENERAL INFORMATION:
; APPLICANT: University of Rochester
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
; TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells
; FILE REFERENCE: 1821.0070004
; CURRENT APPLICATION NUMBER: US/09/987,456
; PRIOR APPLICATION NUMBER: 2001-11-14
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/262,067
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/298,087
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/249,268
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 148
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p 7.5/ATG1/tk promoter
US-09-987-456-3
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```
Query Match
Best Local Similarity 91.0%; Score 132; DB 10; Length 148;
Matches 145; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
Oy 1 GGCCTAAATTTGAAAACATGATCTATTATTGACAGCGCGCCGCTGATCCCCGG 57
Db 1 GGCCTAAATTTGAAAACATGATCTATTATTGACAGCGCGCCGCTGATCCCCGG 60
Oy 58 GGCCTGAGGAATTCGATATCAAGCTTATCGATACCGTGCAGGCGGGGGCGCTAACT 117
Db 61 GGCCTGAGGAATTCGATATCAAGCTTATCGATACCGTGCAGGCGGGGGCGCTAACT 120
Oy 118 AACTAATTTGTTTTGTGTGGCCGCGCC 145
Db 121 AACTAATTTGTTTTGTGTGGCCGCGCC 148
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RESULT 5
US-09-822-250-8
; Sequence 8, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
; CURRENT APPLICATION NUMBER: US/09/822,250
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 149
; TYPE: DNA
; ORGANISM: synthetic construct
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US-09-822-250-8

Query Match	90.3%	Score 131;	DB 10;	Length 149;
Best Local Similarity	97.3%	Pred. No. 4.8e-40;		
Matches 145; Conservative	0;	Mismatches 0;	Indels 4;	Gaps 1;

Qy	1	GGAAAATTTGAAACCTACATCTATTATTGTCAGCGGGCCGCC	---	-TGGATCCCC	56
Db	1	GGCCAAAATTTGAAAACCTAGATCTATTATTATGACCGCGGCCGCATGATGATCCCC			60
Qy	57	GGCGTCGAGGAATTCGATATCACTTATGATTCGCTGCACCTCGAGGGGGGCGCTAAC			116
Db	61	GGCGTCGAGGAATTCGATATCACTTATGATTCGCTGCACCTCGAGGGGGGCGCTAAC			120
Qy	117	TAACTAATTTGTTTGTGTGGCGCGGCC			145
Db	121	TAACTAATTTGTTTGTGTGGCGCGGCC			149

RESULT 6
US-09-987-456-4

	Query Match	90.3%	Score 131;	DB 10;	Length 149;
	Best Local Similarity	97.3%;	Pred. No.	4.8e-40;	
	Matches 145; Conservative	0;	Mismatches	0;	Indels 4; Gaps
QY	1	GGCCAAAATTTGAAAAAAGCTAGATCATATTATTTATTCGCACCGCGGCCGCGC-----GTGCATCCCC	56		
Dd	1	GGCCAAAATTTGAAAAAAGCTAGATCATATTATTTATTCGCACCGCGCGCCGCGCAATGATGATCCCC	60		
QY	57	GGGCTGCAGGAATTCGATTAATCAACCTTATCGATACCGTCGACCTCGAGGGGGGGGCGCTAAC	116		
Dd	61	GGGCTGCAGGAATTCGATTAATCAACCTTATCGATACCGTCGACCTCGAGGGGGGGGCGCTAAC	120		
QY	117	TAACTAATTTTGTTTTGTGTGGCGCCGGCC	145		
Dd	121	TAACTAATTTTGTTTTGTGTGGCGCCGGCC	149		

RESULT 7
US-09-823-250-9
; Sequence 9, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice

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: TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
: FILE REFERENCE: 1821.0010001
: CURRENT APPLICATION NUMBER: US/09/822,250
: CURRENT FILING DATE: 2001-04-02
: PRIOR APPLICATION NUMBER: US 08/935,377
: PRIOR FILING DATE: 1997-09-22
: NUMBER OF SEQ. ID NOS: 37
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 9
: LENGTH: 150
: TYPE: DNA
: ORGANISM: synthetic construct
US-09-822-250-9

Query Match      89.7%; Score 130; DB 10; Length 150;
Best Local Similarity 96.7%; Pred. No. 1,1e-39;
Matches 145; Conservative 0; Mismatches -3; Indels 5; Gaps 1;

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Qy	1	GGCAAAATTTGAAAACTACATCTATTATTTATGACGCGGCGC-----GGTGAATCCCC	55
Db	1	GGCAAAATTTGAAAACTACATCTATTATTTATGACGCGGCGCGCATAGCTGGATCCCC	60
Qy	56	CGGGCTGCAGGAATTCGATCAAGCTTATGATACGGTGCACCTCGAGGGGGGGCCTAA	115
Db	61	CGGGCTGCAGGAATTCGATCAAGCTTATGATACGGTGCACCTCGAGGGGGGGCCTAA	120
Qy	116	CTAACTAATTTTGTTTTGTGGGCGCGGCGC	145
Db	121	CTAACTAATTTTGTTTTGTGGGCGCGGCGC	150

RESULT 8
 US-09-987-456-5
 Sequence 5, Application US/09987456
 Patent No. US20020123057A1
 GENERAL INFORMATION:
 APPLICANT: University of Rochester
 APPLICANT: Zauderer, Maurice
 APPLICANT: Ernest S. Smith
 TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
 TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells
 FILE REFERENCE: 1821.0070004
 CURRENT APPLICATION NUMBER: US/09/987,456
 CURRENT FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: 60/271,424
 PRIOR FILING DATE: 2001-02-27
 PRIOR APPLICATION NUMBER: 60/262,067
 PRIOR FILING DATE: 2001-01-18
 PRIOR APPLICATION NUMBER: 60/298,087
 PRIOR FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: 60/249,268
 PRIOR FILING DATE: 2000-11-17
 NUMBER OF SEQ ID NOS: 147
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 5
 LENGTH: 150
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: p7.5/ATG3/ck vector
 US-09-987-456-5

Query Match	89.7%;	Score 130;	DB 10;	Length 150;
Best Local Similarity	96.7%;	Pred. No. 1.1e-39;		
Matches 145; Conservative	0;	Mismatches	0;	Indels 5; Gaps 1

QY	1	GGCCAAAATTGAAACCTGATCTATTTTATGACGGGGCCG	----	-GTTGGATCC	55
Db	1	GGCCAAAATTGAAACCTGATCTATTTTATGACGGGGCCG	----	-GTTGGATCC	60
QY	56	CGGGCTGCAGGAATTCGATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCCCTAA			115
Db	61	CGGGCTGCAGGAATTCGATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCCCTAA			120


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; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 570, 591, 655, 664, 667, 683, 711, 759, 760, 765, 777, 787,
; LOCATION: 792, 794, 801, 804, 809, 817, 820
; OTHER INFORMATION: n = A,T,C or G
US-09-897-778-91

Query Match
Best Local Similarity 47.3%; Score 68.6; DB 10; Length 858;
Matches 77; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Oy 22 ATCTATTATGCAAGCGGCGCTGATGCCCGGGCTCGAGGAATTCATATCAAGC 81
Db 333 AACGATTCCACACACACGACTGACTGTGATCCCGGGCTCGAGGAATTCATATCAAGC 392
Oy 82 TTATGATACCGTGCACCTCGAGGGGGGCC 112
Db 393 TTATGATACCGTGCACCTCGAGGGGGGCC 423

RESULT 13
US-09-784-130-9/c
; Sequence 9, Application US/09784130
; Patent No. US20020076808A1
; GENERAL INFORMATION:
; APPLICANT: Donahue, Brian A.
; APPLICANT: Hardy, Stephen F.
; APPLICANT: Snyder, Richard O.
; APPLICANT: Cell Genesys, Inc.
; TITLE OF INVENTION: USE OF SUPPRESSOR tRNA'S TO REGULATE CYTOTOXICITY
; FILE REFERENCE: P132222
; CURRENT APPLICATION NUMBER: US/09/784,130
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/097,328
; PRIOR FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 118
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: polylinker
US-09-784-130-9

Query Match
Best Local Similarity 46.2%; Score 67; DB 10; Length 118;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 46 GTGATCCCCCGGCTGAGGAATTCATATCAAGCTTATGATACCGTGCAGC 105
Db 91 GTGATCCCCCGGCTGAGGAATTCATATCAAGCTTATGATACCGTGCAGC 32
Oy 106 GGGGGCC 112
Db 31 GGGGGCC 25

RESULT 14
US-09-735-705-306
; Sequence 306, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
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; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 306
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-735-705-306

Query Match
Best Local Similarity 46.2%; Score 67; DB 10; Length 457;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 46 GTGATCCCCCGGCTGAGGAATTCATATCAAGCTTATGATACCGTGCAGC 105
Db 360 GTGATCCCCCGGCTGAGGAATTCATATCAAGCTTATGATACCGTGCAGC 419
Oy 106 GGGGGCC 112
Db 420 GGGGGCC 426

RESULT 15
US-09-850-716A-306
; Sequence 306, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 306
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-850-716A-306

Query Match
Best Local Similarity 46.2%; Score 67; DB 10; Length 457;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 46 GTGATCCCCCGGCTGAGGAATTCATATCAAGCTTATGATACCGTGCAGC 105
Db 360 GTGATCCCCCGGCTGAGGAATTCATATCAAGCTTATGATACCGTGCAGC 419
Oy 106 GGGGGCC 112
Db 420 GGGGGCC 426

Search completed: November 10, 2002, 11:33:45
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Job time : 38.087 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:43:30 ; Search time 37.1739 Seconds

(Without alignments)
1196.219 Million cell updates/sec

Title: US-08-935-377-6

Perfect score: 145

Sequence: 1 GGCCAAAATTGAAAACCTA.....TTGTTTGTGGCCGCCGCC 145

Scoring table:

IDENTITY_NUC
Gap 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summariesDatabase : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70.4	48.6	5592	4 US-09-495-797-37	Sequence 37, Appl
2	69	47.6	229	4 US-09-116-492A-39	Sequence 39, Appl
3	68.6	47.3	858	4 US-09-123-912-91	Sequence 91, Appl
4	68.6	47.3	858	4 US-09-643-597-91	Sequence 91, Appl
5	68.2	47.0	793	2 US-08-967-101-121	Sequence 121, App
6	68.2	47.0	793	2 US-08-592-541-121	Sequence 121, App
7	68.2	47.0	793	3 US-09-124-698-121	Sequence 121, App
8	68.2	47.0	793	4 US-09-127-480-121	Sequence 121, App
9	68.2	47.0	793	4 US-08-496-841C-121	Sequence 121, App
10	68.2	47.0	793	4 US-09-124-523-121	Sequence 121, App
11	67	46.2	147	4 US-09-323-872A-126	Sequence 121, App
12	67	46.2	457	4 US-09-643-597-306	Sequence 26, Appl
13	67	46.2	752	4 US-08-976-259-108	Sequence 108, App
14	67	46.2	2961	4 US-08-446-935-6	Sequence 6, Appl
15	67	46.2	3792	2 US-08-992-334-1	Sequence 1, Appl
16	67	46.2	3792	2 US-08-302-752-1	Sequence 1, Appl
17	67	46.2	4016	1 US-08-410-540-3	Sequence 3, Appl
18	67	46.2	5234	2 US-08-992-334-2	Sequence 2, Appl
19	67	46.2	5234	3 US-08-302-752-2	Sequence 2, Appl
20	67	46.2	6722	2 US-08-992-334-3	Sequence 3, Appl
21	67	46.2	6722	3 US-08-302-752-3	Sequence 3, Appl
22	66.8	46.1	545	4 US-08-991-789A-10	Sequence 10, Appl
23	66.8	46.1	545	4 US-09-062-451-10	Sequence 10, Appl
24	66.8	46.1	545	4 US-09-588-326-10	Sequence 10, Appl
25	66	45.1	11233	4 US-08-980-832-27	Sequence 27, Appl
26	65.4	45.1	5356	4 US-08-446-935-1	Sequence 1, Appl
27	65.4	45.1	9318	2 US-08-793-610-6	Sequence 6, Appl

C	28	65	44.8	78	4	US-09-462-645C-25	Sequence 25, Appl
	29	65	44.8	84	4	US-09-462-645C-26	Sequence 26, Appl
	30	65	44.8	698	4	US-08-998-416-54	Sequence 54, Appl
	31	65	44.8	3465	4	US-09-462-645C-9	Sequence 9, Appl
	32	65	44.8	3481	4	US-09-462-645C-11	Sequence 11, Appl
	33	65	44.8	3794	4	US-09-462-645C-5	Sequence 5, Appl
	34	65	44.8	3810	4	US-09-462-645C-7	Sequence 7, Appl
	35	65	44.8	6596	4	US-09-575-602-11	Sequence 11, Appl
	36	64.4	44.4	713	4	US-08-998-416-135	Sequence 135, Appl
	37	62.6	43.2	1023	2	US-08-198-446B-1	Sequence 1, Appl
	38	62.6	43.2	1023	2	US-08-870-693-1	Sequence 1, Appl
	39	62.6	43.2	2150	1	US-08-198-446B-10	Sequence 10, Appl
	40	62.6	43.2	2150	2	US-08-870-693-10	Sequence 10, Appl
	41	62.4	43.0	685	1	US-08-463-115-56	Sequence 56, Appl
	42	62.4	43.0	685	1	US-08-465-388-56	Sequence 56, Appl
	43	59	40.7	4164	1	US-08-204-675-1	Sequence 1, Appl
	44	59	40.7	4164	2	US-08-660-754-1	Sequence 1, Appl
	45	59	40.7	4164	2	US-08-796-364-1	Sequence 1, Appl

ALIGNMENTS

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RESULT 1
US-09-495-797-37
; Sequence 37, Application US/09495797
; Patent No. 6369296
; GENERAL INFORMATION:
; APPLICANT: Ratcliff, Frank G
; APPLICANT: Martin-Hernandez, Ana M
; APPLICANT: Baicombe, David C
; TITLE OF INVENTION: Viral Vectors
; FILE REFERENCE: Newburn 43,047
; CURRENT APPLICATION NUMBER: US/09/495,797
; CURRENT FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 5592
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pTV00
US-09-495-797-37

Query Match      48.6%; Score 70.4; DB 4; Length 5592;
Best Local Similarity 79.8%; Pred. No. 1.3e-14;
Matches 83; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 9 ATGGAAGAACTAGATCTATTATTGACAGCGCGCGCGTGGATCCCCGGGCTGACAGAA 68
    ||| || || || || || || || || || || || || || || || || || || || ||
Db 2514 ATTTAAGAGACGTGACACTGTGTGAGATCTTGAACCTAAGTAAGTGAATCCCGCGGCTCAGGAA 2573

QY 69 TTGATATCAAGCTTATTCATACCTGACGCGTCACTGACGAGGGGGGGC 112
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2574 TTGATATCAAGCTTATTCATACCTGACGCGTCACTGACGAGGGGGGGC 2617

RESULT 2
US-09-116-492A-39/C
; Sequence 39, Application US/09116492A
; Patent No. 6436409
; GENERAL INFORMATION:
; APPLICANT: GICOUEL, BRIGITTE
; APPLICANT: BERTHET, FRANCOIS-XAVIER
; APPLICANT: ANDERSEN, PETER
; APPLICANT: RASMUSSEN, PETER B
; TITLE OF INVENTION: POLYNUCLEOTIDE FUNCTIONALLY CODING FOR THE LBP PROTEIN FROM MY
; TITLE OF INVENTION: TUBERCULOSIS, ITS BIOLOGICALLY ACTIVE DERIVATIVE FRAGMENTS, A
; FILE REFERENCE: 0660-0137-27X
; CURRENT APPLICATION NUMBER: US/09/116,492A
; CURRENT FILING DATE: 1998-07-16
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? LOCATION (765)
? OTHER INFORMATION: where n is a, c, g or t
? NAME/KEY: modified_base
? LOCATION: (777)
? OTHER INFORMATION: where n is a, c, g or t
? NAME/KEY: modified_base
? LOCATION: (787)
? OTHER INFORMATION: where n is a, c, g or t
? NAME/KEY: modified_base
? LOCATION: (792)
? OTHER INFORMATION: where n is a, c, g or t
? NAME/KEY: modified_base
? LOCATION: (794)
? OTHER INFORMATION: where n is a, c, g or t
? NAME/KEY: modified_base
? LOCATION: (801)
? OTHER INFORMATION: where n is a, c, g or t
? NAME/KEY: modified_base
? LOCATION: (804)
? OTHER INFORMATION: where n is a, c, g or t
? NAME/KEY: modified_base
? LOCATION: (809)
? OTHER INFORMATION: where n is a, c, g or t
? NAME/KEY: modified_base
? LOCATION: (817)
? OTHER INFORMATION: where n is a, c, g or t
? NAME/KEY: modified_base
? LOCATION: (820)
? OTHER INFORMATION: where n is a, c, g or t
US-09-123-912-91

? Query Match 47.3%, Score 68.6; DB 4; Length 858;
? Best Local Similarity 84.6%; Pred. No. 3,1e-14;
? Matches 77; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 22 ATCTATTATATGACGCGCGCGCGCTGGATCCCCGGGGCTGGAGGATTCGATATCAAGC 81
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DB 333 AACGATTCCACACACAGCTGAGACTAGTGGATCCCGGGGCTCGAGGAATTCATCAAGC 392
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DB 393 TTATCGATACCGCTGCACCTCGAGGGGGGCGC 423
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RESULT 4
US-09-643-597-91
? Sequence 91, Application US/09643597
? Patent No. 6426072
? GENERAL INFORMATION:
? APPLICANT: Wang, Tongtong
? APPLICANT: Fan, Liqun
? APPLICANT: Kalos, Michael D.
? APPLICANT: Bangur, Chaitanya S.
? APPLICANT: Hosken, Nancy
? APPLICANT: Fanger, Gary R.
? APPLICANT: Li, Samuel X.
? APPLICANT: Wang, Aijun
? APPLICANT: Skeiky, Yasir A.W.
? APPLICANT: Henderson, Robert A.
? APPLICANT: McNeill, Patricia D.
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
? TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
? FILE REFERENCE: 210121.455C11
? CURRENT APPLICATION NUMBER: US/09/643,597
? CURRENT FILING DATE: 2000-08-21
? NUMBER OF SEQ ID NOS: 369
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 91
? LENGTH: 858
? TYPE: DNA
? ORGANISM: Homo sapien
? FEATURE:
? NAME/KEY: misc_feature

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,698
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pletcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs.
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-124-698-121

Query Match
Best Local Similarity 47.0%; Score 68.2; DB 3; Length 793;
Matches 76; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
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QY 42 CGCCGTGATCCCCCGGCGTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTC 101
DB 122 CGGGCGGATCCCCCGGCGTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTC 63
QY 102 GAGGGGGGCGCTACTACTATTTGTT 130
DB 62 GAGGGGGGCGCGGTACCCAGCTTTGTT 34
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RESULT 8
US-09-127-480-121/c
Sequence 121, Application US/09127480
Patent No. 6194153
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,480
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pletcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
```

```
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-127-480-121
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Query Match
Best Local Similarity 47.0%; Score 68.2; DB 4; Length 793;
Matches 76; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
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QY 42 CGCCGTGATCCCCCGGCGTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTC 101
DB 122 CGGGCGGATCCCCCGGCGTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTC 63
QY 102 GAGGGGGGCGCTACTACTATTTGTT 130
DB 62 GAGGGGGGCGCGGTACCCAGCTTTGTT 34
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RESULT 9
US-08-496-841C-121/c
Sequence 121, Application US/08496841C
Patent No. 6210919
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
```

```
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,841C
FILING DATE: 28-Jun-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Paul F. Fehner, Ph.D.
REGISTRATION NUMBER: 35,135
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 753-6237
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 121:
US-08-496-841C-121
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Query Match
Best Local Similarity 47.0%; Score 68.2; DB 4; Length 793;
Matches 76; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
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QY 42 CGCCGTGATCCCCCGGCGTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTC 101
DB 122 CGGGCGGATCCCCCGGCGTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTC 63
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; APPLICANT: Dillon, Patrick J.
; APPLICANT: Choi, Gil H.
; APPLICANT: Welch, Rodney A.
; TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli
; Patent No. 6316609
; NUMBER OF SEQUENCES: 142
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,259
; FILING DATE: Herewith
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,626 AND US 60/061,953
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488, 0740002/EKS/CBM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
US-08-976-259-108
Query Match 46.2%; Score 67; DB 4; Length 752;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 GTGATCCCCCGGCTGCAGGATTCGATTCACCTTATCGATCCGTCGACCTCGAGG 105
    |||
DB 72 GTGATCCCCCGGCTGCAGGATTCGATTCACCTTATCGATCCGTCGACCTCGAGG 13
QY 106 GGGGGCC 112
    |||
DB 12 GGGGGCC 6

RESULT 14
US-08-446-935-6/C
; Sequence 6, Application US/08446935
; Patent No. 6187991
; GENERAL INFORMATION:
; APPLICANT: Soeller, Walter C.
; APPLICANT: Carly, Maynard D.
; APPLICANT: Kreuter, David K.
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODELS FOR TYPE II
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pfizer Inc.
; STREET: 235 East 42nd Street, 20th Floor
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10017-5755
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,935
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sheyka, Robert F.
; REGISTRATION NUMBER: 31,304
; REFERENCE/DOCKET NUMBER: PC6153
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)573-1189
; TELEFAX: (212)573-1939
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2961 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
;
US-08-446-935-6
Query Match 46.2%; Score 67; DB 4; Length 2961;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 GTGATCCCCCGGCTGCAGGATTCGATTCACCTTATCGATCCGTCGACCTCGAGG 105
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DB 726 GTGATCCCCCGGCTGCAGGATTCGATTCACCTTATCGATCCGTCGACCTCGAGG 667
QY 106 GGGGGCC 112
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DB 666 GGGGGCC 660

RESULT 15
US-08-992-334-1/C
; Sequence 1, Application US/08992334
; Patent No. 591678
; GENERAL INFORMATION:
; APPLICANT: Gruss, Alexandra
; APPLICANT: Maguin, Emmanuelle
; TITLE OF INVENTION: METHODS FOR USING A TEMPERATURE-SENSITIVE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christie Parker & Hale, LLP
; STREET: 350 West Colorado Boulevard, Suite 500
; CITY: Pasadena
; STATE: California
; COUNTRY: United States
; ZIP: 91105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/992,334
; FILING DATE: 17-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/302,752
; FILING DATE: 24-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR93/00248
; FILING DATE: 12-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/03034
; FILING DATE: 13-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Priout, D. Bruce
```

REGISTRATION NUMBER: 20958
REFERENCE/DOCKET NUMBER: C93:31779
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 795-9900
TELEFAX: (626) 577-8800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3792 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: NO
ANTI-SENSE: YES
IMMEDIATE SOURCE:
CLONE: pc+host4
US-08-992-334-1

Query Match 46.2%; Score 67; DB 2; Length 3792;
Best Local Similarity 100.0%; Pred. No. 1,7e-13;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 GTGGATCCCCCGGCTGCAGAAATCGATATCAAGCTTATCGATACCGTCTGACCTCGAGG 105
|||||
Db 3541 GTGGATCCCCCGGCTGCAGAAATCGATATCAAGCTTATCGATACCGTCTGACCTCGAGG 105
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QY 106 GGGGGCC 112
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Db 3481 GGGGGCC 3475

Search completed: November 10, 2002, 08:36:12
Job time : 40.1739 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:05:45 ; Search time 719.586 Seconds

(without alignments)
5985.683 Million cell updates/sec

Title: US-08-935-377-7

Sequence: 148
1 GGGCCAAAATGAAAACTA.....TTGTTTGTGGGCCCCGCC 148

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb_htg:*
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18: em_in:*
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	148	100.0	148	6 AX326744	AX326744 Sequence
2	137	92.6	149	6 AX326745	AX326745 Sequence
3	136	91.9	150	6 AX326746	AX326746 Sequence
4	132	89.2	145	6 AX326743	AX326743 Sequence
5	70.6	47.7	858	6 AR176413	AR176413 Sequence
6	70.6	47.7	858	6 AX365698	AX365698 Sequence
7	69.8	47.2	259	6 A44281	A44281 Sequence 9
8	69.8	47.2	574	6 AX284736	AX284736 Sequence
9	69.4	46.9	424	6 AX284796	AX284796 Sequence
10	69.4	46.9	2059	12 AY034154	AY034154 Cloning v
11	69.4	46.9	2890	12 AB035274	AB035274 Homo sapi
12	69.4	46.9	2958	6 AX247548	AX247548 Sequence
13	69.4	46.9	2958	12 ARBLKSM	AX2326 Bluescript
14	69.4	46.9	2958	12 ARBLKSP	X52331 Bluescript
15	69.4	46.9	2961	12 ARBLKSM	X52329 Bluescript
16	69.4	46.9	2961	12 ARBLKSP	X52327 Bluescript
17	69.4	46.9	2964	12 SYNBKSMV	L08784 Bluescribe
18	69.4	46.9	2964	12 SYNBKSPV	L08785 Bluescribe
19	69.4	46.9	3306	12 SYNBKSPV	D85525 Cloning vec
20	69.4	46.9	3417	12 AF178449	AF178449 Cloning v
21	69.4	46.9	3485	12 AF178449	AF178449 Integrat
22	69.4	46.9	4144	12 XXU35131	U35131 Plasmid pbs
23	69.4	46.9	4267	12 PRS304	U03436 Yeast integ
24	69.4	46.9	4289	12 XXU35136	U35136 Plasmid pbs
25	69.4	46.9	4373	12 PRS306	U03438 Yeast integ
26	69.4	46.9	4443	12 PRS303	U03435 Yeast integ
27	69.4	46.9	4549	12 AF178452	AF178452 Integrat
28	69.4	46.9	4670	12 ASAU5326	AJ005326 pGAT1(+)
29	69.4	46.9	4670	12 ASAU5329	AJ005329 pGAT1(-)
30	69.4	46.9	4707	12 XXU02374	U02374 Cloning vec
31	69.4	46.9	4768	12 XXU25061	U25061 Cloning vec
32	69.4	46.9	4783	12 PRS314	U03440 Yeast cent
33	69.4	46.9	4887	12 PRS316	U03442 Yeast cent
34	69.4	46.9	4950	12 XXU25060	U25060 Cloning vec
35	69.4	46.9	4967	12 PRS313	U03439 Yeast cent
36	69.4	46.9	5144	12 CVU23751	U23751 Cloning vec
37	69.4	46.9	5187	12 U34687	U34687 Yeast integ
38	69.4	46.9	5228	12 XXU25059	U25059 Cloning vec
39	69.4	46.9	5504	12 PRS305	U03437 Yeast integ
40	69.4	46.9	5634	12 CVU14125	U14125 Cloning vec
41	69.4	46.9	5973	12 AF504908	AF504908 Cloning v
42	69.4	46.9	6018	12 PRS315	U03441 Yeast cent
43	69.4	46.9	6340	12 ASAU5323	AJ005323 pCPI(-) K
44	69.4	46.9	9655	12 SYNPRSV	AD001531 Cloning v
45	68.8	46.5	2961	12 CVU46017	U46017 Cloning vec

ALIGNMENTS

RESULT 1
LOCUS AX326744 148 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 5 from Patent WO0172995.
ACCESSION AX326744
VERSION AX326744.1 GI:18097470
KEYWORDS
SYNOPSIS
SOURCE
ORGANISM
synthetic construct.
synthetic construct.
artificial sequences.
REFERENCE
AUTHORS
TITLE
JOURNAL
Zauderer, M. and Smith, E.S.
Methods of producing a library and methods of selecting
polynucleotides of interest
Patent: WO 0172995-A 5 04-OCR-2001;

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FEATURES
SOURCE
1.148
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Nucleotide Sequence of p7.5/ATG1/Lk"
BASE COUNT
35 a 37 c 39 g 37 t
ORIGIN
Query Match
100.0%; Score 148; DB 6; Length 148;
Best Local Similarity 100.0%; Pred. No. 2.2e-35;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGCAAAATGAAAACATAGATCTATTATTGACGGCGCCGACATGGTGGATCCCCG 60
DB 1 GGGCAAAATGAAAACATAGATCTATTATTGACGGCGCCGACATGGTGGATCCCCG 60
OY 61 GGGTGCAGGAATTCGATATCAAGCTTATTCGATACCGTGCAGGAGGGGGCCTAACT 120
DB 61 GGGTGCAGGAATTCGATATCAAGCTTATTCGATACCGTGCAGGAGGGGGCCTAACT 120
OY 121 AACTAATTTGTTTTGTTGGCCCGGCC 148
DB 121 AACTAATTTGTTTTGTTGGCCCGGCC 148

RESULT 2
AX326745 149 bp DNA linear PAT 07-JAN-2002
LOCUS
DEFINITION
Sequence 6 from Patent WO0172995.
ACCESSION
AX326745
VERSION
AX326745.1 GI:18097471
KEYWORDS
synthetic construct.
synthetic construct.
ORGANISM
artificial sequences.
REFERENCE
1
AUTHORS
Zaederer,M. and Smith,E.S.
TITLE
Methods of producing a library and methods of selecting
polynucleotides of interest
JOURNAL
Patent: WO 0172995-A 6 04-OCT-2001;
UNIVERSITY OF ROCHESTER (US)
FEATURES
Location/Qualifiers
1.149
source
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Nucleotide Sequence of p7.5/ATG2/Lk"
BASE COUNT
36 a 37 c 39 g 37 t
ORIGIN
Query Match
92.6%; Score 137; DB 6; Length 149;
Best Local Similarity 99.3%; Pred. No. 5.9e-37;
Matches 148; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 GGGCAAAATGAAAACATAGATCTATTATTGACGGCGCCGACATGGTGGATCCCC 59
DB 1 GGGCAAAATGAAAACATAGATCTATTATTGACGGCGCCGACATGGTGGATCCCC 60
OY 60 GGGTGCAGGAATTCGATATCAAGCTTATTCGATACCGTGCAGGAGGGGGCCTAACT 119
DB 61 GGGTGCAGGAATTCGATATCAAGCTTATTCGATACCGTGCAGGAGGGGGCCTAACT 120
OY 120 TAACTAATTTGTTTTGTTGGCCCGGCC 148
DB 121 TAACTAATTTGTTTTGTTGGCCCGGCC 149

RESULT 3
AX326746 150 bp DNA linear PAT 07-JAN-2002
LOCUS
DEFINITION
Sequence 7 from Patent WO0172995.
ACCESSION
AX326746
VERSION
AX326746.1 GI:18097472
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KEYWORDS
SOURCE
synthetic construct.
synthetic construct.
ORGANISM
artificial sequences.
REFERENCE
1
AUTHORS
Zaederer,M. and Smith,E.S.
TITLE
Methods of producing a library and methods of selecting
polynucleotides of interest
JOURNAL
Patent: WO 0172995-A 7 04-OCT-2001;
UNIVERSITY OF ROCHESTER (US)
FEATURES
Location/Qualifiers
1.150
source
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Nucleotide Sequence of p7.5/ATG3/Lk"
BASE COUNT
36 a 38 c 39 g 37 t
ORIGIN
Query Match
91.9%; Score 136; DB 6; Length 150;
Best Local Similarity 98.7%; Pred. No. 1.2e-31;
Matches 148; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

OY 1 GGGCAAAATGAAAACATAGATCTATTATTGACGGCGCCGACATG--GTGATCCCC 58
DB 1 GGGCAAAATGAAAACATAGATCTATTATTGACGGCGCCGACATGCGTGAATCCCC 60
OY 59 GGGTGCAGGAATTCGATATCAAGCTTATTCGATACCGTGCAGGAGGGGGCCTAA 118
DB 61 GGGTGCAGGAATTCGATATCAAGCTTATTCGATACCGTGCAGGAGGGGGCCTAA 120
OY 119 CTAATAATTTGTTTTGTTGGCCCGGCC 148
DB 121 CTAATAATTTGTTTTGTTGGCCCGGCC 150

RESULT 4
AX326743 145 bp DNA linear PAT 07-JAN-2002
LOCUS
DEFINITION
Sequence 4 from Patent WO0172995.
ACCESSION
AX326743
VERSION
AX326743.1 GI:18097469
KEYWORDS
synthetic construct.
synthetic construct.
ORGANISM
artificial sequences.
REFERENCE
1
AUTHORS
Zaederer,M. and Smith,E.S.
TITLE
Methods of producing a library and methods of selecting
polynucleotides of interest
JOURNAL
Patent: WO 0172995-A 4 04-OCT-2001;
UNIVERSITY OF ROCHESTER (US)
FEATURES
Location/Qualifiers
1.145
source
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Nucleotide Sequence of p7.5/ATG0/Lk"
BASE COUNT
34 a 37 c 38 g 36 t
ORIGIN
Query Match
89.2%; Score 132; DB 6; Length 145;
Best Local Similarity 98.0%; Pred. No. 2.1e-30;
Matches 145; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

OY 1 GGGCAAAATGAAAACATAGATCTATTATTGACGGCGCCGACATGATGCCCG 60
DB 1 GGGCAAAATGAAAACATAGATCTATTATTGACGGCGCCG--GTGATCCCCG 57
OY 61 GGGTGCAGGAATTCGATATCAAGCTTATTCGATACCGTGCAGGAGGGGGCCTAACT 120
DB 58 GGGTGCAGGAATTCGATATCAAGCTTATTCGATACCGTGCAGGAGGGGGCCTAACT 117
OY 121 AACTAATTTGTTTTGTTGGCCCGGCC 148
|||||
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DB	118	AACTAATTTTGTTTTGTGGGCCGCC	145
RESULT 5	AR176413	858 bp	DNA
LOCUS	AR176413		
DEFINITION	Sequence 91 from patent US 6312695.		Linear
ACCESSION	AR176413		
VERSION	AR176413.1	GI:17918768	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 858)		
TITLE	Reed, S.G. and Wang, T.Tong.		
JOURNAL	Compounds and methods for therapy of lung cancer		
FEATURES	Patent: US 6312695-A 91 06-NOV-2001;		
source	Location/Qualifiers		
	1..858		
BASE COUNT	196 a 212 c 193 g 238 t	19 others	
ORIGIN	1		
Query Match	47.7%: Score 70.6; DB 6; Length 858;		
Best Local Similarity	84.9%: Pred. No. 3.3e-11;		
Matches	79; Conservative 0; Mismatches 14; Indels 0; Gaps 0;		
Qy	23 TCTATTATTGCGCGCGCCCATGTGGATCCCGCGGCTGCAGAAATTCGATATCAA	82	
Db	331 TCAACGAAATTCACACACTGCAGCTGAGTGGATCCCGCGGCTGCAGAAATTCGATATCAA	390	
Qy	83 GCTTATCGATACCGTGCAGCTCGAGGGGGGCC	115	
Db	391 GCTTATCGATACCGTGCAGCTCGAGGGGGGCC	423	
RESULT 6			
LOCUS	AX365698	858 bp	DNA
DEFINITION	Sequence 91 from Patent WO200174.		Linear
ACCESSION	AX365698		
VERSION	AX365698.1	GI:18697250	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1		
AUTHORS	Wang, T., Wang, A., Skelky, Y.A., Li, S.X., Kalos, M.D., Henderson, R.A.,		
	McNeill, P.D., Fanger, N., Retter, M.W., Marnerakis, M., Fanger, G.R.,		
	Vecilic, T.S., Carter, D., Watanabe, Y. and Peckham, D.W.		
TITLE	Compositions and methods for the therapy and diagnosis of Lung		
JOURNAL	cancer		
FEATURES	Patent: WO 0200174-A 91 03-JAN-2002;		
source	Location/Qualifiers		
	1..858		
BASE COUNT	196 a 212 c 193 g 238 t	19 others	
ORIGIN	1		
Query Match	47.7%: Score 70.6; DB 6; Length 858;		
Best Local Similarity	84.9%: Pred. No. 3.3e-11;		
Matches	79; Conservative 0; Mismatches 14; Indels 0; Gaps 0;		
Qy	23 TCTATTATTGCGCGCGCCCATGTGGATCCCGCGGCTGCAGAAATTCGATATCAA	82	
Db	331 TCAACGAAATTCACACACTGCAGCTGAGTGGATCCCGCGGCTGCAGAAATTCGATATCAA	390	
Qy	83 GCTTATCGATACCGTGCAGCTCGAGGGGGGCC	115	
Db	391 GCTTATCGATACCGTGCAGCTCGAGGGGGGCC	423	

RESULT 7	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	BASE COUNT	ORIGIN	Query Match	Best Local Similarity	Matches	Score	DB	Length	Indels	Gaps	Others
7	A44281/c	Sequence 9 from Patent WO9511300.	A44281	A44281.1	GI:2299115	unidentified.	unclassified.	1 (bases 1 to 259)	Chandley,A.C., Kun,M., Sharkey,A.M., Hargreave,T.B. and Cooke,H.J.	AZOOSPERMIA IDENTIFICATION AND TREATMENT	Patent: WO 9511300-A 9 27-APR-1995;	MEDICAL RES COUNCIL (GB)	Other publication AU 7947794 950508.	Location/Qualifiers	1..259	/organism="unidentified"	/db_xref="taxon:32644"	/clone_11b="MOUSE GENOMIC LIBRARY"	67 a	58 c	63 g	69 t	2 others
29	TATGTGACGGGGCCGCGCATGCTGATCCCGGGGCTGCAGGAATTCGATATCAAGCTTAT	88	132	TAAAGGAAGCAAAAGCCTCTAGTGCATCCCGCGGCTGCAGGAATTCGATATCAAGCTTAT	73	CGATACCGTGCAGCTCGAGAGGGGGGCTTAACTAACTAATTTTGT	133	72	CGATACCGTGCAGCTCGAGAGGGGGGCTTAACTAACTAATTTTGT	28	47.2%; Score 69.8; DB 6; Length 259; Pred. 79.0%; Mismatches 0; Indels 22; Gaps 0;												
8	AX284736/c	Sequence 541 from Patent WO0179556.	AX284736	AX284736	AX284736.1	GI:17045424	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	Liilie,J., Brown,J.L., Bolt,A. and van Hufel,C.	Novel genes, compositions and methods for the identification, assessment, prevention, and therapy of human cancers	Patent: WO 0179556-A 541 25-OCT-2001;	Millennium Predictive Medicine, Inc. (US)	Location/Qualifiers	1..574	/organism="Homo sapiens"	/db_xref="taxon:9606"	205 a	150 c	99 g	120 t		
13	AAAAGTACATCTTTTATTCACACGGGGCCGATGGTGAATCCCGGGCTGCAGGAAT	72	134	AACGTTAAATTTACACCTCGGGCGCTCTAATACTAGTGCATCCCGGGCGCGCAGAAC	75	TCGATATCAAGCTTATGATACCGCTGCAGCTCGAGGGGGGCTTAACTAAATTTTGT	132	47.2%; Score 69.8; DB 6; Length 574; Pred. 73.6%; Mismatches 0; Indels 32; Gaps 0;															

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/organism="Cloning vector pIDN4"  
/db_xref="taxon:161273"
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RESULT	11				
AB035274					
LOCUS		2890 bp	mRNA	linear	PRI 12-JUL-2006
DEFINITION	Homo sapiens mRNA for postreplication repair protein hRAD18p,				
ACCESSION	AB035274				
VERSION	AB035274				
KEYWORDS	AB035274.1	GI:8980616			
SOURCE	Homo sapiens placenta cDNA to mRNA.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	1 (sites)				
AUTHORS	Tateishi,S., Sakuraba,Y., Masuyama,S., Inoue,H. and Yanaiizumi,M.				
TITLE	Dysfunction of human Rad18 results in defective postreplication				
JOURNAL	repair and hypersensitivity to multiple mutagens				
MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7927-7932 (2000)				
	20345089				

REFERENCE 2 (bases 1 to 2890)
AUTHORS Tateishi, S., Yamazumi, M. and Inoue, H.
TITLE Direct Submission
JOURNAL Submitted (26-NOV-1999) Satoshi Tateishi, Kumamoto University,
Institute of Molecular Embryology, Kohonji 4-24-1, Kumamoto,
Kumamoto 862-0976, Japan (E-mail: tateigo@kumamoto-u.ac.jp,
Tel:81-096-373-6602, Fax:81-096-373-6604)
FEATURES
SOURCE Location/Qualifiers
1..2890
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/tissue-type="placenta"
1..2890
/gene="hRAD18"
126..1613
/gene="hRAD18"
/note="RING-zinc-finger protein"
/codon_start=1
/product="postreplication repair protein hRAD18p"
/protein_id="BA99284.1"
/db_xref="GI:8980617"
ORIGIN
BASE COUNT 916 a 585 c 601 g 788 t
Query Match 46.9%; Score 69.4; DB 9; Length 2890;
Best Local Similarity 87.4%; Pred. No. 9.5e-11;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 47 TGGTGGATCCCCGGGCTGAGGAATTGATCAAGCTTATGACCGTGCACCTCGA 106
1 |||||||
Db 2740 TAGTGGATCCCCGGGCTGAGGAATTGATCAAGCTTATGACCGTGCACCTCGA 2799
QY 107 GGGGGGCGCTAACTAATTGTTT 133
1 |||||||
Db 2800 GGGGGGCGCGGTACCGACTTTGTT 2826
RESULT 12
LOCUS AX247548 2958 bp DNA Linear PAT 28-SEP-2001
DEFINITION Sequence 1 from Patent WO0166775.
ACCESSION AX247548
VERSION AX247548.1 GI:15862240
KEYWORDS
SOURCE
ORGANISM synthetic construct.
artificial sequence.
1 (bases 1 to 2958)
REFERENCE
AUTHORS Evans, D.H., Miller, D.O. and Yao, X.D.
TITLE Dna joining method
JOURNAL Patent: WO 0166775-A 1 13-SEP-2001;
University of Guelph (CA)
FEATURES
SOURCE Location/Qualifiers
1..2958
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="pDW101"
BASE COUNT 748 a 735 c 752 g 723 t
ORIGIN
Query Match 46.9%; Score 69.4; DB 6; Length 2958;
Best Local Similarity 87.4%; Pred. No. 9.5e-11;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 47 TGGTGGATCCCCGGGCTGAGGAATTGATCAAGCTTATGACCGTGCACCTCGA 106
1 |||||||
Db 682 TAGTGGATCCCCGGGCTGAGGAATTGATCAAGCTTATGACCGTGCACCTCGA 741
QY 107 GGGGGGCGCTAACTAATTGTTT 133
1 |||||||
Db 742 GGGGGGCGCGGTACCGACTTTGTT 768
RESULT 13
ARBLKSP
LOCUS ARBLKSP 2958 bp DNA circular SYN 29-JAN-2002
DEFINITION pBluescript KS(-) vector DNA, phagemid excised from lambda ZAP.
ACCESSION X52326
VERSION X52326.1 GI:58064
KEYWORDS artificial sequence; cloning vector; expression vector; vector.
SOURCE synthetic construct.
ORGANISM synthetic construct.
artificial sequences.
REFERENCE
AUTHORS Short, J.M., Fernandez, J.M., Sorge, J.A. and Huse, W.D.
TITLE Lambda ZAP: a bacteriophage lambda expression vector with in vivo
excision properties
Nucleic Acids Res. 16 (15), 7583-7600 (1988)
JOURNAL MEDLINE 88119944
PUBMED 2970625
REFERENCE
AUTHORS Ailing-Mees, M.A. and Short, J.M.
TITLE pBluescript II: gene mapping vectors
Nucleic Acids Res. 17 (22), 9494 (1989)
JOURNAL MEDLINE 90067967
PUBMED 2553794
REFERENCE
AUTHORS Thomas, E.A.
TITLE Direct Submision
JOURNAL Submitted (20-FEB-1990) Thomas E.A., Stratagene Clonin Systems,
1109 North Torrey Pines Rd., La Jolla, CA 92037, USA
FEATURES
SOURCE Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
misc_feature 1..2958
BASE COUNT 708 a 754 c 731 g 765 t
ORIGIN
Query Match 46.9%; Score 69.4; DB 12; Length 2958;
Best Local Similarity 87.4%; Pred. No. 9.5e-11;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 47 TGGTGGATCCCCGGGCTGAGGAATTGATCAAGCTTATGACCGTGCACCTCGA 106
1 |||||||
Db 685 TAGTGGATCCCCGGGCTGAGGAATTGATCAAGCTTATGACCGTGCACCTCGA 744
QY 107 GGGGGGCGCTAACTAATTGTTT 133
1 |||||||
Db 745 GGGGGGCGCGGTACCGACTTTGTT 771
RESULT 14
ARBLKSP
LOCUS ARBLKSP 2958 bp DNA circular SYN 29-JAN-2002
DEFINITION pBluescript KS(+) vector DNA, phagemid excised from lambda ZAP.
ACCESSION X52331
VERSION X52331.1 GI:58065
KEYWORDS artificial sequence; cloning vector; expression vector; vector.
SOURCE synthetic construct.
ORGANISM synthetic construct.
artificial sequences.
REFERENCE
AUTHORS Short, J.M., Fernandez, J.M., Sorge, J.A. and Huse, W.D.
TITLE Lambda ZAP: a bacteriophage lambda expression vector with in vivo

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FEATURES                                Location/Qualifiers
      source                            1..2961
                                           /organism="synthetic construct"
                                           /db_xref="taxon:32630"
misc_feature                           1..2961
                                           /note="Phagemid pBluescriptII KS(-)"

BASE COUNT          706 a         758 c        735 g       762 t
ORIGIN

Query Match                               46.9%; Score 69.4; DB 12; Length 2961;
Best Local Similarity 87.4%; Pred No. 9, Se-ll;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY . 47 TGTGATCCCCCGGGCTGCAGGAATTGATATCAAGCTTATCATACCGTCGACTCGA 106
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   685 TAGTGATGCCCGGGCTGCAGGAATTGATATCAAGTTATCATACCGTCGACTCGA 744

QY 107 GGGGGGGCCTTACTAACTAATTTGTT 133
    ||||| | | | | | | | | | | | | |
Db 745 GGGGGGGCCCGGTACCACAGCTTTGTT 771

Search completed: November 10, 2002, 06:52:56
Job time : 721.586 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:42:15 ; Search time 1332 Seconds

(without alignments)
1799.499 Million cell updates/sec

Title: US-08-935-377-7

Sequence: 1 GGGCAAAATGAAAAACAT.....TTGTTTGTGGCCCGGCC 148

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST: *
1: em_estda: *
2: em_estln: *
3: em_estln: *
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5: em_estln: *
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7: em_estln: *
8: em_estln: *
9: gb_est1: *
10: gb_est2: *
11: gb_est3: *
12: gb_est4: *
13: gb_est5: *
14: gb_est6: *
15: em_estfun: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_pln: *
21: em_gss_vrt: *
22: em_gss_fun: *
23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rnd: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	75.8	51.2	891	14	BQ140386 NF035A10P
2	72.4	48.9	182	13	B1306115 NL_3_G09
3	72.4	48.9	793	14	BQ143916 NF038H04D
4	71.6	48.4	721	17	CNS06DOU
5	70.4	47.6	682	17	AO074693 CIT-HSP-2
6	70.2	47.4	804	14	BQ158468 NF058H09P

	C	7	70	47.3	728	10	AM682547	EST01410
	C	8	69.8	47.2	182	13	B1305962	B1305962 NL_2_R23
	C	9	69.8	47.2	186	13	B1305695	B1305695 NL_1_G23
	C	10	69.8	47.2	188	17	CNS06049	AL415375 T7 end of
	C	11	69.6	47.0	198	17	CNS06X01	AL419128 T7 end of
	C	12	69.4	46.9	162	10	BE428068	BE428068 MTD002.H1
	C	13	69.4	46.9	390	9	AU234451	AU234451
	C	14	69.4	46.9	400	9	AU234451	AU234451
	C	15	69.4	46.9	912	17	AO937400	AO937400 NB2-011 H
	C	16	69.4	46.9	864	17	CNS06065	AL415767 T7 end of
	C	17	69.2	46.8	175	13	B1306167	B1306167 NL_3_J08
	C	18	69.2	46.8	182	13	B1306149	B1306149 NL_3_J07
	C	19	69.2	46.8	182	13	B1306159	B1306159 NL_3_J12
	C	20	69.2	46.8	182	13	B1306178	B1306178 NL_3_K05
	C	21	69.2	46.8	182	13	B1306180	B1306180 NL_3_K07
	C	22	69.2	46.8	757	14	B0155148	B0155148 NF076611T
	C	23	68.8	46.5	674	10	AV681474	AV681474 AV681474
	C	24	68.8	46.5	776	10	AV681505	AV681505 AV681505
	C	25	68.8	46.5	786	10	AV681504	AV681504 AV681504
	C	26	68.8	46.5	802	10	AV681486	AV681486 AV681486
	C	27	68.8	46.5	806	10	AV681464	AV681464 AV681464
	C	28	68.8	46.5	818	17	CNS060RU	AL416224 T7 end of
	C	29	68.4	46.2	295	10	BE428455	BE428455 MTD007.CO
	C	30	68.4	46.2	608	17	AO009167	AO009167 CIT-HSP-2
	C	31	68.2	46.1	829	17	AO937397	AO937397 NB2-006 H
	C	32	68.2	45.9	928	17	CNS06W2E	AL417900 T7 end of
	C	33	67.8	45.8	528	17	B69688	B69688 CIT978SK-A-
	C	34	67.6	45.7	107	13	BM398556	BM398556 5009-0-47
	C	35	67.6	45.7	211	17	CNS06CB9	AL392299 T7 end of
	C	36	67.4	45.5	108	10	BE492551	BE492551 WHE0554.C
	C	37	67.4	45.5	108	17	B54292	B54292 CIT-HSP-201
	C	38	67.4	45.5	124	10	AM914179	AM914179 EST345483
	C	39	67.4	45.5	128	17	CNS07GJ4	AL609826 Anophelis
	C	40	67.4	45.5	141	9	AU037147	AU037147
	C	41	67.4	45.5	141	17	B95279	B95279 CIT-HSP-217
	C	42	67.4	45.5	144	17	B80294	B80294 CIT-HSP-204
	C	43	67.4	45.5	157	12	BR281431	BR281431 EST446022
	C	44	67.4	45.5	169	13	B1306719	B1306719 NL_5_N23
	C	45	67.4	45.5	169	17	AO013235	AO013235 CIT-HSP-2

ALIGNMENTS

RESULT 1
BQ140386 891 bp mRNA linear EST 26-APR-2002
LOCUS NF035A10PH1F1081 Phoma-infected Medicago truncatula CDNA clone
DEFINITION NF035A10PH 5', mRNA sequence.
ACCESSION BQ140386
VERSION BQ140386.1 GI:20276512
KEYWORDS
SOURCE
ORGANISM
barrel medic.
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
1 (bases 1 to 891)
REFERENCE
AUTHORS Watson,B.S., Shih,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R.,
Gonzales,R.A., Bell,C.J., Imman,J.T., Maugh,M.E., Sullivan,J.P.,
May,G.D. and Paiva,N.L.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula Phoma-infected library
Unpublished (2002)
Contact: Paiva NL
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7317
Fax: 580 221 7380
Email: nlpaiva@noble.org
Insert Length: 891 Std Error: 0.00


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Db      83 TAGTGATATCCCCGGGCGCTAGCAATTCATATCAAGCTTATGATACCGTGACCTCGA 142
QY      107 GGGGGGGCCTAACTAACTAATT 128
Db      143 GGGGGGGCGCCGAGTACCAAT 164

RESULT 4
CNS06D0U
LOCUS   721 bp      DNA      linear      GSS 05-APR-2001
DEFINITION T7 end of clone AROAA014H10 of library AROAA from strain CBS 732 of
            Zygosaccharomyces rouxii, genomic survey sequence.
ACCESSION AL394084
VERSION   AL394084.1 GI:12144845
KEYWORDS  GSS; clone AROAA014H10; RST AROAA014H10CPL.
SOURCE    Zygosaccharomyces rouxii.
           Zygosaccharomyces rouxii.
           Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
           Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces.
REFERENCE 1 (bases 1 to 721)
AUTHORS   Soucieu,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
           Boitlin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
           de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Liorente,B.,
           Malpertuy,A., Neveuglise,C., Ozler-Kalogeropoulos,O., Potier,S.,
           Saurin,M., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
           Winkler,P. and Weissenbach,J.
           Genomic exploration of the hemiascomycetous yeasts: 1. A set of
           yeast species for molecular evolution studies
JOURNAL   FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE   20584711
PUBMED    11152876
TITLE     2 (bases 1 to 721)
           de Montigny,J., Straub,M., Potier,S., Tekala,F., Dujon,B.,
           Winkler,P., Artiguenave,F. and Soucieu,J.
           Genomic exploration of the hemiascomycetous yeasts: 8.
           Zygosaccharomyces rouxii
JOURNAL   FEBS Lett. 487 (1), 52-55 (2000)
MEDLINE   20584718
PUBMED    11152883
TITLE     3 (bases 1 to 721)
           Genoscope.
           Direct Submission
           Submitted (28-MAR-2001) Genoscope - Centre National de Sequencage,
           2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
           sequef@genoscope.cns.fr Web : www.genoscope.cns.fr)
           This BAC end sequence is part of a random genomic sequencing
           program of thirteen yeast species:
           . Saccharomyces bayanus var. uvarum,
           . Saccharomyces exiguus,
           . Saccharomyces servazii,
           . Zygosaccharomyces rouxii,
           . Saccharomyces kluyveri,
           . Kluyveromyces thermotolerans,
           . Kluyveromyces lactis var. lactis,
           . Kluyveromyces marxianus var. marxianus
           . Pichia angusta,
           . Debaryomyces hansenii var. hansenii,
           . Pichia sorbitophila,
           . Candida tropicalis and
           . Yarrowia lipolytica.
           Genomic inserts of 3 to 5 kb were prepared and both extremities
           were sequenced. See keywords for description of this sequence and
           for the sequence of the other extremity of this insert.
FEATURES
source    Location/Qualifiers
           1..721
           /organism="Zygosaccharomyces rouxii"
           /strain="CBS 732"
           /db_xref="taxon:4956"
           /clone="AROAA014H10"
           /clone_1id="AR0A"
           /note="end : T7"

BASE COUNT      188 a      100 c      201 g      193 t      39 others

```

```

ORIGIN
Query Match      48.4%; Score 71.6; DB 17; Length 721;
Best Local Similarity 81.4%; Pred. No. 8.4e-13;
Matches 83; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY      14 AAAACTGATCTATTATTCGACGCGCCCGCATGTGATCCCCGGGCTGCAGCAATT 73
Db      215 ATACTTATGTTTATTTATTCATGATAGCCAGCTGATCCCCGGGCTGCAGCAATT 274

QY      74 CGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCC 115
Db      275 CGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCC 316

RESULT 5
A0074693/c
LOCUS    A0074693      682 bp      DNA      linear      GSS 20-AUG-1998
DEFINITION CTT-HSP-2301L23.TF CTT-HSP Homo sapiens genomic clone 2301L23, DNA
            sequence.
ACCESSION A0074693
VERSION   A0074693.1 GI:3436811
KEYWORDS  GSS.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 682)
AUTHORS   Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
           Berry,K., Granger,D., Sub,E., Wible,C., Shizuya,H., Simon,M. and
           Venter,J.C.
           Use of a random human BAC End Sequence Database for Sequence-Ready
           Map Building
           Unpublished (1998)
           Contact: Mark Adams
           Department of Eukaryotic Genomics
           The Institute for Genomic Research
           9712 Medical Center Dr., Rockville, MD 20850, USA
           Tel: 301 838 0200
           Fax: 301 838 0208
           Email: mdadams@tigr.org
           Clones are available from Research Genetics (info@resgen.com). BAC
           end search page:
           http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html.
           Seq primer: M13-21
           Class: BAC ends.
FEATURES
source    Location/Qualifiers
           1..682
           /organism="Homo sapiens"
           /db_xref="taxon:9606"
           /clone="2301L23"
           /clone_1id="CTT-HSP"
           /sex="Male"
           /cell_type="Sperm"
           /note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
           HindIII"

BASE COUNT      156 a      187 c      187 g      151 t      1 others

ORIGIN
Query Match      47.6%; Score 70.4; DB 17; Length 682;
Best Local Similarity 92.5%; Pred. No. 2.1e-12;
Matches 74; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      47 TGGTGATCCCGCGGCGCTGAGCAATTCGATATCAAGCTTATGATACCGTCGACCTCGA 106
Db      80 TAGTGATATCCCCGGGCGCTAGCAATTCATATCAAGCTTATGATACCGTCGACCTCGA 21

QY      107 GGGGGGGCCTAACTAACTAA 126
Db      20 GGGGGGGCGCCGAGTACCA 1

RESULT 6

```

LOCUS	B0158468	804 bp	mRNA	linear	EST 24-APR-2002
DEFINITION	NF05BH09PLJ1078 Phosphate starved leaf Medicago truncatula cDNA clone NF05BH09PL 5', mRNA sequence.				
ACCESSION	B0158468				
VERSION	B0158468.1	GI:20295525			
KEYWORDS	EST.				
SOURCE	barrel medic.				
ORGANISM	Medicago truncatula				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.				
AUTHORS	1 (bases 1 to 804) Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Jman,J.T., Weller,J.W., May,G.D. and Harrison,M.J. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula phosphate-starved leaf library Unpublished (2000)				
JOURNAL	Contact: Harrison MJ Plant Biology Division The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7325 Fax: 580 221 7380				
COMMENT	Email: mjharrison@noble.org Insert Length: 804 Std Error: 0.00 Plate: 058 row: H column: 09 Seq primer: TCACACAGGAACAAGCATATGAC. Location/Qualifiers 1..804				
FEATURES	/organism="Medicago truncatula" /db_xref="taxon:3880" /clone="NF05BH09PL" /clone_id="phosphate starved leaf" /tissue_type="leaf" /dev_stage="trifoliolate" /note="Vector: Lambda Zap; At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 20mM potassium phosphate. RNA was prepared from above ground tissues."				
BASE COUNT	215 a 202 c 181 g 165 t	41 others			
ORIGIN					
Query Match	47.4%	Score 70.2;	DB 14;	Length 804;	
Best Local Similarity	88.2%;	Fred. No. 2.4e-12;			
Matches	75;	Conservative 0;	Mismatches 10;	Indels 0;	Gaps 0;
OY	47 TGGTGGATCCCCCGGGGTGCAGAAATTGCATTCAGCTTATCGATACGCTGACTCGA	106			
I					
Db	80 TAGTGGAATCCCGGGGCTCAGCAATTCGATNCAAGCTTATCGATACCGCTGNACCTCGA	139			
I					
OY	107 GGGGGGCCCTTAACATAATTTTG	131			
I					
Db	140 GGGGGGGCCCTGTACCCCAATTCTG	164			
I					
RESULT 7					
AM682547/c	728 bp mRNA linear EST 14-APR-2000				
LOCUS	AM682547	E8.5 mouse craniofacial subregion cDNA library Mus musculus cDNA clone e064, mRNA sequence.			
DEFINITION					
ACCESSION	AM682547				
VERSION	AM682547.1	GI:7557255			
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 728) Murakami,Y., Li,H., Chowdhury,S., Yamada,K.M. and Yamada,Y.				
AUTHORS					

FEATURES	source	1. .728	/organism="Mus musculus"	
COMMENT			/strain="ICR"	
			/db_xref="taxon:10090"	
			/clone="e064"	
			/clone_lib="E8.5 mouse craniofacial subtraction CDNA library"	
			/tissue_type="craniofacial tissues"	
			/dev_stage="embryonic day 8.5"	
			/note="Vector: pT-Adv; A subtraction CDNA library was constructed from E8.5 mouse craniofacial mRNA subtraced from E13.5 mouse craniofacial mRNA."	
BASE COUNT	191 a	158 c	179 g	188 t
ORIGIN				12 others
Query Match		47.3%	Score 70;	DB 10; Length 728;
Best Local Similarity		80.4%;	Pred. No. 2.8e-12;	
Matches	82; Conservative	0;	Mismatches 20;	Indels 0; Gaps 0;
QY	42	CGCCATGGTGAATCCCGGGGCTGGAGAGAAATTCAGATCAACTATGATACCGTCGAC	101	
Db	117	CTCGAGGGGGGATCCCGGGGCTGCGAGGAATTCGATATCAACTATGATACCGTCGAC	58	
QY	102	CTCGAGGGGGGGCTAACTAACTAATTTTGTGTTTGTGGGCC	143	
Db	57	CTCGAGGGGGGGCCGCTACCAATTCGCCCTATATGATGGGCC	16	
RESULT 8				
BI305962/c		BI305962	182 bp	mRNA linear EST 20-JUL-2001
LOCUS		NI_2_K23	Drought stress (leaf)	Oryza sativa cDNA clone NI_2_K23 3'
DEFINITION			mRNA sequence.	
ACCESSION		BI305962		
VERSION		BI305962.1	GI:14981284	
KEYWORDS		EST.		
SOURCE		Oryza sativa.		
ORGANISM		Oryza sativa		
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS		Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
		Ehmerioideae; Oryzaceae; Oryza.		
TITLE		1 (bases 1 to 182)		
JOURNAL		Reddy,A.R., Ramakrishna,W., Chandrasekhar,A., Nagabushan,I.,		
COMMENT		Ravindrababu,P. and Bennetzen,J.L.		
		Novel EST enrichment with normalized cDNA libraries from drought		
		stressed rice (Oryza sativa L.cv Nagina 22)		
		Unpublished (2001)		
		Contact: Reddy AR		
		Department of Plant Sciences, School of Life Sciences		
		University of Hyderabad		
		P.O. Central University, Hyderabad-500 046, A.P, India		
		Tel: 0091-40-3010265		
		Fax: 0091-40-3010145		
		Email: arjuls@uohyd.ernet.in		
		Insert Length: 182	Std Error: 0.00	
		Plate: 2	row: K	column: 23
		Seq primer: GTAAACGACGGCGAGTG.		
		Location/Qualifiers		
		1. .182		
FEATURES		/organism="Oryza sativa"		
source		/cultivar="Nagina 22 (indica sub sp)"		

[illegible]

QY	107	GGGGGGGCGCTACTACTAATT 128
Db	53	GGGGGGGCGCGCTACCAATT 32
RESULT 10		
CNS06049		
LOCUS		
DEFINITION		188 bp DNA linear GSS 05-JUL-2001
ACCESSION		TF end of clone AX0AA004H12 of library AX0AA from strain CBS 7064
VERSION		AL15375
KEYWORDS		AL15375.1 GI:12194520
SOURCE		GSS.
ORGANISM		<i>Pichia farinosa</i> .
REFERENCE		<i>Pichia farinosa</i> .
AUTHORS		Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; <i>Pichia</i> .
TITLE		1 (bases 1 to 188)
JOURNAL		Soucié, J. L., Aigle, M., Artiguenave, F., Blandin, G., Boloiti, F., Kulara, M., Bon, E., Brotier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durand, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuvéglise, C., Ozler-Kalogeropoulos, O., Potier, S., Saurin, M., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.
MEDLINE		Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
PUBMED		FEBS Lett. 487 (1), 3-12 (2000)
REFERENCE		2 (bases 1 to 188)
AUTHORS		de Montigny, J., Spohner, C., Soucié, J., Tekala, F., Dujon, B., Wincker, P., Artiguenave, F. and Potier, S.
TITLE		Genomic exploration of the hemiascomycetous yeasts: 15. <i>Pichia sorbitophila</i>
JOURNAL		FEBS Lett. 487 (1), 87-90 (2000)
MEDLINE		20584725
PUBMED		11152890
REFERENCE		3 (bases 1 to 188)
AUTHORS		Genoscope.
TITLE		Direct Submission
JOURNAL		Submitted (07-SEP-2000) Genoscope - Centre National de Séquençage, 2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)
MEDLINE		This GSS is part of a random genomic sequencing program of thirteen yeast species: <i>Saccharomyces bayanus</i> var. <i>uvaturum</i> , <i>Saccharomyces exiguus</i> , <i>Saccharomyces servazzii</i> , <i>Zygosaccharomyces rouxii</i> , <i>Saccharomyces kluyveri</i> , <i>Kluyveromyces thermotolerans</i> , <i>Kluyveromyces lactis</i> var. <i>lactis</i> , <i>Kluyveromyces marxianus</i> var. <i>marxianus</i> , <i>Pichia angusta</i> , <i>Debaryomyces hansenii</i> var. <i>hansenii</i> , <i>Pichia sorbitophila</i> , <i>Candida tropicalis</i> and <i>Yarrowia lipolytica</i> . Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
COMMENT		Location/Qualifiers
		1..188
FEATURES		/organism="Pichia farinosa"
source		/strain="CBS 7064"
		/db_xref="taxon:4920"
		/clone="AX0AA004H12"
		/clone_11b="AX0AA"
		/note="end : 17"
BASE COUNT		48 a 40 c 59 g 40 t 1 others
ORIGIN		
Query Match		47.2%; Score 69.8; DB 17; Length 188;
Best Local Similarity		91.4%; Pred. No. 3.4e-12;
Matches		74; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY	35	ACGGGCGCCGATGGTGGATCCCCGGGCTCAGAGATTCATATCAAGCTTATCGATAC 94
Db	75	AGGAGGGGCAAGAGATATCCCGGGCTCCAGAGATTCATATCAAGCTTATCGATAC 134

QY	95	CGTCGACCTCGAGGGGGGCC	115
Db	135	CGTCGACCTCGAGGGGGGCC	155

RESULT 11	LOCUS	DEFINITION
CNS06X01	198 bp DNA	linear GSS 06-JUL-2001
CNS06X01	T7 end of clone AX0AA037A11 of library AX0A from strain CBS 7064 of <i>Pichia farinosa</i> , genomic survey sequence.	

REFERENCE	AUTHORS
1 (pages 1 to 199)	Soucié,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S., de-Montigny,J., Dujein,B., Durans,P., Lepingle,A., Llorente,B., Malpeyrou,A., Neufange,C., Ozier-Kalopoulos,O., Pottier,S., Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.
TITLE	Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
JOURNAL	FEBS Lett. 487 (1), 3-12 (2000)

JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Séquençage
2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
sege@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This GSS is part of a random genomic sequencing program of thirteen
yeast species: *Saccharomyces bayanus* var. *varium*, *Saccharomyces*
exiguus, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*,
Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces*
lactis var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia*
angusta, *Debaryomyces hansenii* var. *hansenii*, *Pichia soboloffii*, *La-*
Candida tropicalis and *Yarrowia lipolytica*. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.

BASE COUNT	42 a	59 c	54 g	4.1 t	2 others
ORIGIN					

Oy 40 GCCCGCATGTGGATCCCGGCGCTGCAGGAATTGCATTACGATACCCTCG 99
111 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 104 GCCTTCAGCTGGATCCCCGGGCTGCAGGAATTGCATTACGATACCCTCG 163

QY 100 ACCTGGAGGGGGGCC 115

Db 164 ACCTCGAGGGGGGCC 179

RESULT 12	BE428068	162 bp	mRNA	linear	EST 26-JUL-2000
LOCUS	BE428068				
DEFINITION	MTD002.H10F990615 ITCC MTD durum Wheat Root Library Trilicium				
	turgidum subsp. durum cDNA clone MTD002.H10, mRNA sequence.				
ACCESSION	BE428068				
VERSION	BE428068.1	GI:9425911			

REFERENCE
1 (bases 1 to 162)
Anderson O.A., Appels R., Bailey P., Blake T., Close T., Cloutier
S., Dubcovsky T., Feuillet C., Gale M., Graner A., Gustafson P.,
Herrmann R.G., Holton T., Jacquemont J.M., Jan J., Joudrier P.,
Langridge P., Izzo G.R., Lin J.F., McGuire P., Ogihara T.,
Pecchioni N., Qualset C., Schuch W., Selvaraj G., Shariflou M.,
Sorrells M., Warburton M. and Wenzel G.
International Triticeae EST Cooperative (IREC): Production of
Expressed Sequence Tags for Species of the Triticeae
Unpublished (2000)
Joudrier P.

International Triticeae EST Cooperative (ITEC)
<http://wheat.pw.usda.gov/genome>.
 Location/Qualifiers

BASE COUNT	28 a	42 c	49 g	43 t
ORIGIN				
Query Match		46.9%;	Score 69.4;	DB 10; Length 162;
Best Local Similarity		87.4%;	Pred. NO.4,6e.12;	
Matches	76;	Conservative	0;	Mismatches 11; Indels 0; Gaps 0;

QY	47 TGTGATGCCCGGGCTGCAGGAATTGATATCAAGTTCATACCGTGACCTCGA	106
Dd	22 TAGTGATGCCCGGGCTGCAGGAATTGATATCAAGTTCATACCGTGACCTCGA	81
QY	107 GGGGGGGCCTAACTAACTAATTTTGT	133
Dd	82 GGGGGGGCCGGTAGCCAGCTTTGTT	108

2Y	107	GGGGGGGCTACTACTAATTTTGT	133
Db	82	GGGGGGCGGTACCAAGCTTTGTT	108

RESULT 13	AU234451	390 bp	mRNA	linear	EST 21-SEP-2001
LOCUS	AU234451				
DEFINITION	AU234451 Bovine placenta cDNA Bos taurus cDNA clone Cln153', mRNA sequence.				

```

XX PS Disclosure; Fig 2; 132pp; English.
XX CC
XX CC The present sequence represents a fragment of a vaccinia transfer
XX CC plasmid, which is used in the course of the invention. The
XX CC specification describes a method for identifying a target epitope.
XX CC The method comprises screening the products of an expression library
XX CC from a cell expressing the target epitope with cytotoxic T cells
XX CC generated against the cell to identify DNA clones expressing the target
XX CC epitope. The method may also comprise providing a cytotoxic T cell
XX CC specific for a gene product differentially expressed by a cell and
XX CC measuring the cross-reactivity of the cytotoxic T cell. The methods are
XX CC useful for identifying tumour specific target epitopes and antigens which
XX CC are useful in immunogenic compositions or vaccines to induce the
XX CC regression of tumours, cancers or infections in mammals. The genes
XX CC expressed in a panel of tumour cells that are derived from single
XX CC immortalised, non-tumorigenic cell line are used to generate HLA
XX CC restricted cytotoxic T cells which are evaluated for activity against
XX CC tumour cells. The method is useful to identify potential antigens
XX CC expressed not only by the pathogen but also by the host cells whose gene
XX CC expression is altered as a result of infection. The differential gene
XX CC expression strategies can be applied to identify immunogenic molecules
XX CC of cells infected with virus, fungus or mycobacterium.
XX SQ
XX Sequence 148 BP; 35 A; 37 C; 39 G; 37 T; 0 other;
XX
Query Match          100.0%; Score 148; DB 21; Length 148;
Best Local Similarity 100.0%; Pred. No. 2.5e-41;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGCACAAAATGAAAACTAGATCTATTATTGACACGCGCGCCGCGATGTGATCCCCG 60
    |||||||
DB 1 GGCACAAAATGAAAACTAGATCTATTATTGACACGCGCGCGCGATGTGATCCCCG 60
QY 61 GCGTCGACGAATTGCATATCAAGCTTATCCATACCGTCGACCTGAGGGGGGCGCTACT 120
    |||||||
DB 61 GCGTCGACGAATTGCATATCAAGCTTATCCATACCGTCGACCTGAGGGGGGCGCTACT 120
QY 121 AACTAATTTGTTTGTGCGGCCGCC 148
    |||||||
DB 121 AACTAATTTGTTTGTGCGGCCGCC 148

RESULT 2
ABA01477
ID ABA01477 standard; DNA; 148 BP.
XX
AC ABA01477;
XX
DT 04-FEB-2002 (first entry)
XX
DE Partial p7.5/ATG1/Lk sequence.
XX
KW Cell death; toxic gene; tumour suppressor; ds.
XX
OS Synthetic.
XX
PN W0200172995-A2.
XX
PD 04-OCT-2001.
XX
PF 28-MAR-2001; 2001WO-US09953.
XX
PR 28-MAR-2000; 2000US-0192586.
PR 10-MAY-2000; 2000US-0203343.
PR 23-JAN-2001; 2001US-0263226.
PR 27-FEB-2001; 2001US-0271426.
XX
PA (UVRP ) UNIV ROCHESTER.
XX
PI Zauderer M, Smith ES;
XX
DR WPI; 2001;570897/64.

```

```

XX PS Selecting target polynucleotides, particularly toxic genes, involves
XX PT introducing a library of insert polynucleotides into a host cell
XX PT population, where the target polynucleotide promotes cell death -
XX PS Disclosure; Fig 8; 359pp; English.
XX CC
XX CC The present invention relates to a method for selecting a target
XX CC polynucleotide. The method comprises introducing into a host cell
XX CC population a library of insert polynucleotides, where expression of the
XX CC target polynucleotide directly or indirectly promotes host cell death.
XX CC The cells are cultured and the insert polynucleotides are collected from
XX CC the cells which die. The method is useful for selecting target
XX CC polynucleotides, particularly polynucleotides which alter cell phenotypes
XX CC of induce or inhibit cell death. The method can be used to isolate toxic
XX CC genes such as tumour suppressors. The present sequence was used to
XX CC illustrate the method of the the present invention.
XX SQ
XX Sequence 148 BP; 35 A; 37 C; 39 G; 37 T; 0 other;
XX
Query Match          100.0%; Score 148; DB 22; Length 148;
Best Local Similarity 100.0%; Pred. No. 2.5e-41;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGCACAAAATGAAAACTAGATCTATTATTGACACGCGCGCCGCGATGTGATCCCCG 60
    |||||||
DB 1 GGCACAAAATGAAAACTAGATCTATTATTGACACGCGCGCGCGCGATGTGATCCCCG 60
QY 61 GCGTCGACGAATTGCATATCAAGCTTATCCATACCGTCGACCTGAGGGGGGCGCTACT 120
    |||||||
DB 61 GCGTCGACGAATTGCATATCAAGCTTATCCATACCGTCGACCTGAGGGGGGCGCTACT 120
QY 121 AACTAATTTGTTTGTGCGGCCGCC 148
    |||||||
DB 121 AACTAATTTGTTTGTGCGGCCGCC 148

RESULT 3
AAD31779
ID AAD31779 standard; DNA; 148 BP.
XX
AC AAD31779;
XX
DT 18-JUN-2002 (first entry)
XX
DE Modified p7.5/Lk vector, p7.5/ATG1/Lk.
XX
KW Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;
KW vaccine; immune response; cytostatic; p7.5/Lk vector; thymidine kinase;
XX
OS Vaccinia virus.
XX
OS Synthetic.
XX
FH Key
FH FT misc_signal
    Location/Qualifiers
    /tag= a
    /note= "Translation start codon"
    116..118
    /tag= b
    /note= "Translation stop codon"
    120..122
    /tag= c
    /note= "Translation stop codon"
    124..126
    /tag= d
    /note= "Translation stop codon"
    132..138
    /tag= e
    /note= "Transcription stop signal"
XX
XX US2002018785-A1.

```



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XX Cell death; toxic gene; tumour suppressor; ds.
XX Synthetic.
OS
XX WO200172995-A2.
XX
XX 04-OCT-2001.
XX
XX 28-MAR-2001; 2001WO-US09953.
XX
XX 28-MAR-2000; 2000US-0192586.
XX 10-MAY-2000; 2000US-0203343.
XX 23-JAN-2001; 2001US-0263226.
XX 27-FEB-2001; 2001US-0271426.
XX
XX (UVRP ) UNIV ROCHESTER.
XX
XX Zauderer M, Smith ES;
XX
XX WPI; 2001-570897/64.
XX
XX Selecting target polynucleotides, particularly toxic genes, involves
XX introducing a library of insert polynucleotides into a host cell
XX population, where the target polynucleotide promotes cell death -
XX
XX Disclosure; Fig 8; 359pp; English.
XX
XX The present invention relates to a method for selecting a target
XX polynucleotide. The method comprises introducing into a host cell
XX a population a library of insert polynucleotides, where expression of the
XX target polynucleotide directly or indirectly promotes host cell death.
XX The cells are cultured and the insert polynucleotides are collected from
XX the cells which die. The method is useful for selecting target
XX polynucleotides, particularly polynucleotides which alter cell phenotypes
XX of induce or inhibit cell death. The method can be used to isolate toxic
XX genes such as tumour suppressors. The present sequence was used to
XX illustrate the method of the the present invention.
XX
XX Sequence 149 BP; 36 A; 37 C; 39 G; 37 T; 0 other;
XX
XX Query Match 92.6%; Score 137; DB 22; Length 149;
XX Best Local Similarity 99.3%; Pred. No. 1.6e-37;
XX Matches 148; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
XX 1 GGGCAAAATTTGAAACCTAGATCTATTATTTATGACGCGCGCCCATG-GTGGATCCCC 59
XX |
XX 1 GGGCAAAATTTGAAACCTAGATCTATTATTTATGACGCGCGCCCATGATGATCCCC 60
XX
XX 60 GGGCTGCAGAAATTCATCAAGCTTATGATACCGTGCAGCTCGAGGGGGGCTTAC 119
XX |
XX 61 GGGCTGCAGAAATTCATCAAGCTTATGATACCGTGCAGCTCGAGGGGGGCTTAC 120
XX
XX 120 TAACTATTGTTGTTTGTGGCGCCGCC 148
XX |
XX 121 TAACTAATTTTGTGTTGTGGCGCCGCC 149
XX
XX
XX RESULT 6
XX AD31780
XX ID AD31780 standard; DNA: 149 BP.
XX
XX AAD31780;
XX
XX 18-JUN-2002 (first entry)
XX
XX Modified p7.5/lk vector, p7.5/ATG2/lk.
XX
XX Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;
XX vaccine; immune response; cytostatic; p7.5/lk vector; thymidine kinase;
XX p7.5/ATG2/lk vector; ds.
XX
XX Vaccinia virus.
XX

```

```

OS Synthetic.
XX
XX Key Location/Qualifiers
XX misc_signal 46..48
XX /*tag= a
XX /note= "Translation start codon"
XX 117..119
XX /*tag= b
XX /note= "Translation stop codon"
XX 121..123
XX /*tag= c
XX /note= "Translation stop codon"
XX 125..127
XX /*tag= d
XX /note= "Translation stop codon"
XX 133..139
XX /*tag= e
XX /note= "Transcription stop signal"
XX
XX US2002018785-A1.
XX
XX 14-FEB-2002.
XX
XX 02-APR-2001; 2001US-0822250.
XX
XX 22-SEP-1997; 97US-0935377.
XX
XX (UVRP ) UNIV ROCHESTER.
XX
XX Zauderer M;
XX
XX WPI; 2002-239252/29.
XX
XX Representative Difference Analysis method for identification of
XX antigens recognized by cytotoxic T cells and specific for human tumors,
XX comprises improved selection of genes encoding target antigens -
XX
XX Example 1; Fig 2; 54pp; English.
XX
XX The present invention relates to novel methods for the identification
XX of antigens recognised by cytotoxic T cells (CTLs) and specific for
XX human tumors, cancers and infected cells. The method involves screening
XX the products of an expression library generated from DNA/RNA of a cell
XX expressing a target epitope with cytotoxic T cells generated against
XX the cell to identify DNA clones expressing target epitope or providing
XX cytotoxic T cells specific for a gene product differentially expressed
XX by a cell and measuring the cross-reactivity of the cytotoxic T cells
XX for cells expressing a target epitope in which the target epitope is
XX identified as a gene product inducing cytotoxic T cells. The method is
XX useful for identifying a target epitope or antigen specific for a tumour
XX cell. The target epitope is also useful for identifying target antigens
XX in other target cells against which it is desirable to induce cell-
XX mediated immunity. The antigen identified by the method is useful
XX in immunogenic compositions and vaccine preparations to induce the
XX regression of tumours, cancers and infections in mammals. The invention
XX also relates to vaccinia viral vectors which are useful for treating
XX tumour-bearing mammals, including humans to generate immune response
XX against the tumour cells. They are also useful for immunising or
XX vaccinating tumour-free subjects to prevent tumour formation. The
XX present sequence is modified p7.5/lk (thymidine kinase) vector,
XX p7.5/ATG2/lk. This vector comprises a vaccinia virus 7.5K promoter and
XX a modified tk DNA fragment. This vector is used in the exemplification
XX of the invention.
XX
XX Sequence 149 BP; 36 A; 37 C; 39 G; 37 T; 0 other;
XX
XX Query Match 92.6%; Score 137; DB 24; Length 149;
XX Best Local Similarity 99.3%; Pred. No. 1.6e-37;
XX Matches 148; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
XX 1 GGGCAAAATTTGAAACCTAGATCTATTATTTATGACGCGCGCCCATG-GTGGATCCCC 59
XX |
XX 1 GGGCAAAATTTGAAACCTAGATCTATTATTTATGACGCGCGCCCATGAGTGAATCCCC 60
XX

```


Qy	60	GGGCTGAGGAATTGCATATCAGCTTATGATACCGTCGACCTCGAGGGGGGCGCTAAC	119
Db	61	GGGCTGAGGAATTGCATATCAGCTTATGATACCGTCGACCTCGAGGGGGGCGCTAAC	120
Qy	120	TAACTAATTTTGTTTTGTGGCCCGGCC	148
Db	121	TAACTAATTTTGTTTTGTGGCCCGGCC	149
RESULT 7			
AAAI5238			
ID	AAAI5238	standard; DNA; 150 BP.	
XX	AAAI5238;		
AC			
XX			
DT	04-SEP-2000	(first entry)	
XX			
DE		Nucleotide sequence of a fragment of the plasmid p7.5/ATG3/tk.	
XX			
KM		Vaccinia transfer plasmid; epitope; tumour specific epitope; antigen;	
XX		vaccine; tumour regression; cancer; infection; ss.	
OS		Synthetic.	
XX			
PN	WO200028016-A1.		
XX			
PD	18-MAY-2000.		
XX			
PF	10-NOV-1998;	98WO-US24029.	
XX			
PR	10-NOV-1998;	98WO-US24029.	
XX			
PA	(UYRP) UNIV ROCHESTER.		
XX			
PI	Zauderer M;		
XX			
DR	WPI: 2000-376533/32.		
XX			
PT		Novel method of identifying target epitopes or antigens specific for	
PT		human tumors, cancers and infected cells involving screening expression	
PT		library products of a cell expressing the target epitope	
XX			
PS		Disclosure: Fig 2; 132pp; English.	
XX			
CC		The present sequence represents a fragment of a vaccinia transfer	
CC		plasmid, which is used in the course of the invention. The	
CC		specification describes a method for identifying a target epitope.	
CC		The method comprises screening the products of an expression library	
CC		from a cell expressing the target epitope with cytotoxic T cells	
CC		generated against the cell to identify DNA clones expressing the target	
CC		epitope. The method may also comprise providing a cytotoxic T cell	
CC		specific for a gene product differentially expressed by a cell and	
CC		measuring the cross-reactivity of the cytotoxic T cell. The methods are	
CC		useful for identifying tumour specific target epitopes and antigens which	
CC		are useful in immunogenic compositions or vaccines to induce the	
CC		regression of tumors, cancers or infections in mammals. The genes	
CC		expressed in a panel of tumour cells that are derived from single	
CC		immortalised, non-tumourigenic cell line are used to generate hTA	
CC		restricted cytotoxic T cells which are evaluated for activity against	
CC		tumour cells. The method is useful to identify potential antigens	
CC		expressed not only by the pathogen but also by the host cells whose gene	
CC		expression is altered as a result of infection. The differential gene	
CC		expression strategies can be applied to identify immunogenic molecules	
CC		of cells infected with virus, fungus or mycobacterium.	
XX			
XX			
Seq	Sequence 150 BP; 36 A; 38 C; 39 G; 37 T; 0 other;		
Qy			
Query Match	91.9%;	Score 136; DB 21; Length 150;	
Best Local Similarity	98.7%;	Pred. No. 3-5e-37;	
Matches 148; Conservative	0; Mismatches	0; Indels	2; Gaps
1	GGCCAAATTTGAATAACATGATCTATTATTGACACGGCGCCGCAATG--GTGATATCCCC	58	

Db	1	GGCCAAAANTGAAAACTGATCTATTTATTTGACGGCCGCCCATGACGTGGATCCCC	60
QY	59	CGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCTTAA	118
Db	61	CGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCTTAA	120
QY	119	CTAAGTAATTTGTTTGTGGGGCCGCC	148
Db	121	CTAAGTAATTTGTTTGTGGGGCCGCC	150
RESULT 8			
ID	ABA01479	standard; DNA; 150 BP.	
AC	ABA01479;		
XX			
DT	04-FEB-2002 (first entry)		
XX			
DE	Partial p7.5/ATG3/tlx sequence.		
XX			
KW	Cell death; toxic gene; tumour suppressor; ds.		
XX			
OS	Synthetic.		
XX			
PN	WO200172995-A2.		
XX			
PD	04-OCT-2001.		
XX			
PF	28-MAR-2001; 2001WO-US09953.		
XX			
PR	28-MAR-2000; 2000US-0192586.		
XX			
PR	10-MAY-2000; 2000US-0203343.		
XX			
PR	23-JAN-2001; 2001US-0263226.		
XX			
PR	27-FEB-2001; 2001US-0271426.		
XX			
FA	(UTRP) UNITV ROCHESTER.		
XX			
PI	Zauderer M, Smith ES;		
XX			
DR	WPI; 2001-570897/64.		
XX			
PT	Selecting target polynucleotides, particularly toxic genes, involves		
XX			
PT	introducing a library of insert polynucleotides into a host cell		
XX			
PT	population, where the target polynucleotide promotes cell death -		
XX			
PS	Disclosure; Fig 8; 359pp; English.		
XX			
CC	The present invention relates to a method for selecting a target		
XX			
CC	polynucleotide. The method comprises introducing into a host cell		
XX			
CC	population a library of insert polynucleotides, where expression of the		
XX			
CC	target polynucleotide directly or indirectly promotes host cell death.		
XX			
CC	The cells are cultured and the insert polynucleotides are collected from		
XX			
CC	the cells which die. The method is useful for selecting target		
XX			
CC	polynucleotides, particularly polynucleotides which alter cell phenotypes		
XX			
CC	of induce or inhibit cell death. The method can be used to isolate toxic		
XX			
CC	genes such as tumour suppressors. The present sequence was used to		
XX			
CC	illustrate the method of the present invention.		
XX			
SQ	Sequence 150 BP; 36 A; 38 C; 39 G; 37 T; 0 other;		
Query Match			
Best Local Similarity 98.7%; Score 136; DB 22; Length 150;			
Matches 148; Conservative 0; Mismatches 0; Indels 2; Gaps 1;			
QY	1	GGCCAAAANTGAAAACTGATCTATTTATTTGACGGCCGCCCATG- -GNGGATCCCC	58
Db	1	GGCCAAAANTGAAAACTGATCTATTTATTTGACGGCCGCCCATGACGTGGATCCCC	60
QY	59	CGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCTTAA	118
Db	61	CGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCTTAA	120

Oy	119	CTAACTAATTTGTTTGTGGGCCCCGGCC	148
Db	121	CTAACTAATTTGTTTGTGGGCCCCGGCC	150
RESULT 9			
ID	AAD31781	standard; DNA; 150 BP.	
XX			
AC	AAD31781;		
XX			
DF	18-JUN-2002	(first entry)	
XX			
DE	Modified p7.5/tk vector, p7.5/ATG3/tk.		
XX			
XX	Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;		
KW	vaccine; immune response; cytostatic; p7.5/tk vector; thymidine kinase;		
KW	p7.5/ATG3/tk vector; ds.		
XX			
OS	Vaccinia virus.		
XX	Synthetic.		
FH	Key	Location/Qualifiers	
FT	misc_signal	46..48	
FT		/tag= a	
FT		/note= "translation start codon"	
FT	misc_signal	118..120	
FT		/tag= b	
FT		/note= "translation stop codon"	
FT	misc_signal	122..124	
FT		/tag= c	
FT		/note= "translation stop codon"	
FT	misc_signal	126..128	
FT		/tag= d	
FT		/note= "translation stop codon"	
FT	misc_signal	134..140	
FT		/tag= e	
FT		/note= "transcription stop signal"	
XX			
PN	US2002018785-A1.		
XX			
XX	14-FEB-2002.		
PD			
XX			
PF	02-APR-2001; 2001US-0822250.		
XX			
PR	22-SEP-1997; 97US-0935377.		
XX			
PA	(UYRP) UNIV ROCHESTER.		
XX			
PI	Zauderer M;		
XX			
DR	WPI; 2002-239252/29.		
XX			
PT	Representational Difference Analysis method for identification of		
PT	antigens recognized by cytotoxic T cells and specific for human tumours,		
PT	comprises improved selection of genes encoding target antigens -		
XX			
PS	Example 1; Fig 2; 54pp; English.		
XX			
XX	The present invention relates to novel methods for the identification		
CC	of antigens recognised by cytotoxic T cells (CTLs) and specific for		
CC	human tumours, cancers and infected cells. The method involves screening		
CC	the products of an expression library generated from DNA/RNA of a cell		
CC	expressing a target epitope with cytotoxic T cells generated against		
CC	the cell to identify DNA clones expressing target epitope or providing		
CC	cytotoxic T cells specific for a gene product differentially expressed		
CC	by a cell and measuring the cross-reactivity of the cytotoxic T cells		
CC	for cells expressing a target epitope in which the target epitope is		
CC	identified as a gene product inducing cytotoxic T cells. The method is		
CC	useful for identifying a target epitope or antigen specific for a tumour		
CC	cell. The target epitope is also useful for identifying target antigens		
CC	in other target cells against which it is desirable to induce cell-		

CC	mediated immunity. The antigen identified by the method is useful
CC	in immunogenic compositions and vaccine preparations to induce the
CC	regression of tumours, cancers and infections in mammals. The invention
CC	also relates to vaccinia viral vectors which are useful for treating
CC	tumour-bearing mammals, including humans to generate immune response
CC	against the tumour cells. They are also useful for immunising or
CC	vaccinating tumour-free subjects to prevent tumour formation. The
CC	present sequence is modified p7.5/tk (thymidine kinase) vector,
CC	p7.5/ANG3/tk. This vector comprises a vaccinia virus 7.5K promoter and
CC	a modified tk DNA fragment. This vector is used in the exemplification
CC	of the invention.
XX	
XX	Sequence 150 BP; 36 A; 38 C; 39 G; 37 T; 0 other;
XX	
XX	Query Match 91.9%; Score 136; DB 24; Length 150;
XX	Best Local Similarity 98.7%; Pred. No. 3.5e-37;
XX	Matches 148; Conservative 0; Mismatches 0; Indels 2; Gaps
XX	
QY	1 GGGCAAAAATTGAAAACACTAGATCTATTATTATTTGACACGGCGCGCCGATG-6TGATATCCC 58
DB	1 GGGCAAAAATTGAAAACACTAGATCTATTATTATTTGACACGGCGCGCCATACGTGATCCCC 60
QY	59 CGGGCTGCAGGAATTCGATATCAGCTTATGATACCGTCGACCTCGAGGGGGGACCTAA 118
DB	61 CGGGCTGCAGGAATTCGATATCAGCTTATGATACCGTCGACCTCGAGGGGGGACCTAA 120
QY	119 CTAACTAATTTTGTTTTGTGTGGGCCCGGCC 148
DB	121 CTAACTAATTTTGTTTTGTGTGGGCCCGGCC 150
XX	
XX	RESULT 10
XX	AAAI5235
XX	AAAI5235 standard; DNA; 145 BP.
XX	AAAI5235;
XX	04-SEP-2000 (first entry)
XX	
DE	Nucleotide sequence of a fragment of the plasmid p7.5/ANG0/tk.
XX	
KW	Vaccinia transfer plasmid; epitope; tumour specific epitope; antigen;
KW	vaccine; tumour regression; cancer; infection; ss.
XX	
OS	Synthetic.
XX	
PN	WO200028016-A1.
PD	18-MAY-2000.
XX	
XX	10-NOV-1998; 98WO-US24029.
XX	
PR	10-NOV-1998; 98WO-US24029.
XX	
PA	(UYP) UNIV ROCHESTER.
XX	
PI	Zauderer M;
XX	
DR	WPI: 2000-376533/32.
XX	
PT	Novel method of identifying target epitopes of antigens specific for
PT	human tumors, cancers and infected cells involving screening expression
XX	library products of a cell expressing the target epitope -
XX	
PS	Disclosure; Fig 2; 132pp; English.
XX	
CC	The present sequence represents a fragment of a vaccinia transfer
CC	plasmid, which is used in the course of the invention. The
CC	specification describes a method for identifying a target epitope.
CC	The method comprises screening the products of an expression library
CC	from a cell expressing the target epitope with cytotoxic T cells
CC	generated against the cell to identify DNA clones expressing the target
CC	epitope. The method may also comprise providing a cytotoxic T cell

16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PI Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 8499, 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 658 BP; 176 A; 151 C; 164 G; 167 T; 0 other;
XX
Query Match 51.9%; Score 76.8; DB 23; Length 658;
Best Local Similarity 75.0%; Pred. No. 1.6e-16;
Matches 96; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 6 AAATTTGAAAACCTAGATCTATTATTGACGCGCGCCCATGTGTGATCCCCGGGCTG 65
DB 484 AATATTAGTTCCTCCAGATCTGTACCTCGCGCCCTAGAACTAGTGTGATCCCCGGGCTG 543
QY 66 CAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTGAGGGGGGGCCCTACTACTA 125
DB 544 CAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTGAGGGGGGGCCCGGTACCCAG 603
QY 126 ATTTTGT 133
DB 604 CTTTGT 611
XX
RESULT 15
ABV41330
ID ABV41330 standard; cDNA; 671 BP.
XX
XX ABV41330;
AC
XX
XX 16-SEP-2002 (first entry)
DE
XX
XX Human prostate expression marker cDNA 41321.
DE
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
XX WO200160860-A2.
PN
XX
XX 23-AUG-2001.
PD
XX
XX 20-FEB-2001; 2001WO-US05171.
PF

XX
XX 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PI Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 8309-8310, 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 671 BP; 181 A; 153 C; 167 G; 170 T; 0 other;
XX
Query Match 51.9%; Score 76.8; DB 23; Length 671;
Best Local Similarity 75.0%; Pred. No. 1.6e-16;
Matches 96; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 6 AAATTTGAAAACCTAGATCTATTATTGACGCGCGCCCATGTGTGATCCCCGGGCTG 65
DB 498 AATATTAGTTCCTCCAGATCTGTACCTCGCGCCCTAGAACTAGTGTGATCCCCGGGCTG 557
QY 66 CAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTGAGGGGGGGCCCTACTACTA 125
DB 558 CAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTGAGGGGGGGCCCGGTACCCAG 617
QY 126 ATTTTGT 133
DB 618 CTTTGT 625
XX

Search completed: November 10, 2002, 05:58:28
Job time : 175.627 secs

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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:58:40 ; Search time 36.8336 Seconds
(without alignments)
1425.554 Million cell updates/sec

Title: US-08-935-377-7
Perfect score: 148
Sequence: 1 GGCCAAAAATTGAAAACTA.....TTGTTTTCGTGGCCCGGCC 148

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 320260 seqs, 177392727 residues

Total number of hits satisfying chosen parameters: 640520

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 08

Listing first 45 summaries

Database : Published_Applications_NA:

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1: /cgn2_6/p/odataa/1/pubna/US07_PUBCOMB.seq.*
2: /cgn2_6/p/odataa/1/pubna/PCU1_NEW_PUB.seq.*
3: /cgn2_6/p/odataa/1/pubna/US06_NEW_PUB.seq.*
4: /cgn2_6/p/odataa/1/pubna/US06_NEW_PUB.seq.*
5: /cgn2_6/p/odataa/1/pubna/US06_PUBCOMB.seq.*
6: /cgn2_6/p/odataa/1/pubna/PCUUS_PUBCOMB.seq.*
7: /cgn2_6/p/odataa/1/pubna/US08_NEW_PUB.seq.*
8: /cgn2_6/p/odataa/1/pubna/US08_PUBCOMB.seq.*
9: /cgn2_6/p/odataa/1/pubna/US09_NEW_PUB.seq.*
10: /cgn2_6/p/odataa/1/pubna/US09_PUBCOMB.seq.*
11: /cgn2_6/p/odataa/1/pubna/US10_NEW_PUB.seq.*
12: /cgn2_6/p/odataa/1/pubna/US10_PUBCOMB.seq.*
13: /cgn2_6/p/odataa/1/pubna/US60_NEW_PUB.seq.*
14: /cgn2_6/p/odataa/1/pubna/US60_PUBCOMB.seq.*

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	148	100.0	148	10	US-09-822-250-7	Sequence 7, Appl1
2	148	100.0	148	10	US-09-987-456-3	Sequence 3, Appl1
3	137	92.6	149	10	US-09-822-250-8	Sequence 8, Appl1
4	137	92.6	149	10	US-09-987-456-4	Sequence 4, Appl1
5	136	91.9	150	10	US-09-822-250-9	Sequence 9, Appl1
6	136	91.9	150	10	US-09-987-456-5	Sequence 5, Appl1
7	132	89.2	145	10	US-09-822-250-6	Sequence 6, Appl1
8	132	89.2	145	10	US-09-987-456-2	Sequence 2, Appl1
9	70.6	49.7	858	10	US-09-735-705-01	Sequence 91, Appl1
10	70.6	47.7	858	10	US-09-850-716A-91	Sequence 91, Appl1
11	70.6	47.7	858	10	US-09-887-778-91	Sequence 91, Appl1
12	69.8	47.2	574	10	US-09-834-575-541	Sequence 541, Appl1
13	69.4	46.9	424	10	US-09-834-575-601	Sequence 601, Appl1
14	67.4	45.3	118	10	US-09-784-130-9	Sequence 9, Appl1
15	67.4	45.5	457	10	US-09-735-705-306	Sequence 306, Appl1
16	67.4	45.5	457	10	US-09-850-716A-306	Sequence 306, Appl1
17	67.4	45.5	457	10	US-09-897-778-306	Sequence 306, Appl1
18	67.4	45.5	752	10	US-09-956-004-108	Sequence 108, Appl1
19	67.2	45.4	545	10	US-09-810-936-10	Sequence 10, Appl1

C	20	67.2	45.4	545	10	US-09-429-757-16	Sequence 10, Appl
C	21	67.2	45.4	661	10	US-09-912-447-16	Sequence 16, Appl
C	22	62	41.9	103	10	US-09-974-300-7717	Sequence 7717, Ap
C	23	60.4	40.8	62	10	US-09-854-923-1	Sequence 1, Appl1
C	24	55.2	37.3	624	10	US-09-834-975-469	Sequence 469, Appl
C	25	54	36.5	1094	10	US-09-932-118-3	Sequence 3, Appl1
C	26	52.2	35.3	4633	10	US-09-880-107-3822	Sequence 3822, Ap
C	27	50.4	34.1	586	10	US-09-924-0335-701	Sequence 701, Appl
C	28	49.8	34.6	1981	10	US-09-408-222-26	Sequence 26, Appl
C	29	48.8	33.6	6244	10	US-09-281-674-8	Sequence 8, Appl1
C	30	48.8	33.6	6244	10	US-09-692-227-8	Sequence 8, Appl1
C	31	48.6	33.6	332	10	US-09-823-114-14	Sequence 14, Appl
C	32	49.4	33.4	343	10	US-09-924-0358-839	Sequence 839, Appl
C	33	49	33.1	53	10	US-09-822-250-23	Sequence 23, Appl
C	34	49	33.1	57	10	US-09-822-250-5	Sequence 5, Appl1
C	35	49	33.1	57	10	US-09-887-456-1	Sequence 1, Appl1
C	36	49	33.1	69	10	US-09-822-250-1	Sequence 1, Appl1
C	37	49	33.1	69	10	US-09-887-456-1	Sequence 1, Appl1
C	38	49	33.1	1329	10	US-09-887-456-140	Sequence 140, Appl
C	39	49	33.1	1329	10	US-09-925-959-240	Sequence 240, Appl
C	40	49	33.1	2790	10	US-09-739-254-30	Sequence 30, Appl
C	41	48.4	32.7	100	10	US-09-904-615-30	Sequence 30, Appl
C	42	48	32.4	57	10	US-09-380-7284-19	Sequence 19, Appl
C	43	48	32.4	57	10	US-09-955-649-4	Sequence 4, Appl1
C	44	48	32.4	362	10	US-09-973-013-4	Sequence 4, Appl1
C	45	47.4	32.0	341	10	US-09-925-300-903	Sequence 903, Appl
						US-09-735-705-302	Sequence 302, Appl

ALIGNMENTS

```

RESULT 1
US-09-822-250-7
: Sequence 7, Application US/09822250
: Patent No. US20020018785A1
: GENERAL INFORMATION:
: APPLICANT: Zauderer, Maurice
: TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
: FILE REFERENCE: 1821.0010001
: CURRENT APPLICATION NUMBER: US/09/822,250
: CURRENT FILING DATE: 2001-04-02
: PRIOR APPLICATION NUMBER: US 08/935,377
: PRIOR FILING DATE: 1997-09-22
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: Patentin version 3.0
: SEQ ID NO 7
: LENGTH: 148
: TYPE: DNA
: ORGANISM: synthetic construct
: US-09-822-250-7

```

Query Match	100.0%;	Score 148;	DB 10;	Length 148;
Best Local Similarity	100.0%;	Pred. No. 3.8e-47;		
Matches 148;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	GGCAAAATTTAAAAACTATATCTATTTTTCACGGGGCCCATGGTGGATCCCCG	60
Db	1	GGCAAAATTTAAAAAAGTATCTATTTTTCACGGGGCCCGCCATGGTGGATCCCCG	60
Qy	1	GGCAAAATTTAAAAAAGTATCTATTTTTCACGGGGCCCGCCATGGTGGATCCCCG	60
Db	1	GGCAAAATTTAAAAAAGTATCTATTTTTCACGGGGCCCGCCATGGTGGATCCCCG	60
Qy	61	GGCTGAGGAATTCATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCTAACT	120
Db	61	GGCTGAGGAATTCATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCTAACT	120
Qy	61	GGCTGAGGAATTCATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCTAACT	120
Db	61	GGCTGAGGAATTCATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCTAACT	120
Qy	121	AACTAATTTTGTGTTTGCGGGCCGGCC	148
Db	121	AACTAATTTTGTGTTTGCGGGCCGGCC	148
Qy	121	AACTAATTTTGTGTTTGCGGGCCGGCC	148
Db	121	AACTAATTTTGTGTTTGCGGGCCGGCC	148

RESULT 2
US-09-987-456-3
; Sequence 3, Application US/09987456
; Patent No. US20020123057A1
; GENERAL INFORMATION:

```

; APPLICANT: University of Rochester
; APPLICANT: Zauderer, Maurice
; APPLICANT: Ernest S. Smith
; TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
; TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells
; FILE REFERENCE: 1821.0070004
; CURRENT APPLICATION NUMBER: US/09/987,456
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/271,424
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/262,067
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/298,087
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/249,268
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 148
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p 7.5/ATG1/tk promoter
US-09-987-456-3

```

```

Query Match          100.0%; Score 148; DB 10; Length 148;
Best Local Similarity 100.0%; Pred. No. 3,8e-47;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GGGCAAAATTTGAAAACATGATCTATTTATTTGACAGCGGCCCATGTGATCCCGG 60
    |||||||
DB 1 GGGCAAAATTTGAAAACATGATCTATTTATTTGACAGCGGCCCATGTGATCCCGG 60
    |||||||
QY 61 GGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTTCAGCCCTCGAGGGGGCCTTA 120
    |||||||
DB 61 GGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTTCAGCCCTCGAGGGGGCCTTA 120
    |||||||
QY 121 AACTAATTTGTTTGTGGGGCCGGCC 148
    |||||||
DB 121 AACTAATTTGTTTGTGGGGCCGGCC 148
    |||||||

```

```

RESULT 3
US-09-822-250-8
; Sequence 8, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
; CURRENT APPLICATION NUMBER: US/09/822,250
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 149
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-822-250-8

```

```

Query Match          92.6%; Score 137; DB 10; Length 149;
Best Local Similarity 99.3%; Pred. No. 6,1e-43;
Matches 148; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```

```

QY 1 GGGCAAAATTTGAAAACATGATCTATTTATTTGACAGCGGCCCATG-GTGAATCCCG 59
    4|||||
DB 1 GGGCAAAATTTGAAAACATGATCTATTTATTTGACAGCGGCCCATGAGTGAATCCCG 60
    |||||||
QY 60 GGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTTCAGCCCTCGAGGGGGCCTTA 119
    |||||||

```

```

DB 61 GGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTTCAGCCCTCGAGGGGGCCTTA 120
QY 120 TAATAATTTGTTTGTGGGGCCGGCC 148
    |||||||
DB 121 TAATAATTTGTTTGTGGGGCCGGCC 149
    |||||||

```

```

RESULT 4
US-09-987-456-4
; Sequence 4, Application US/09987456
; Patent No. US20020123057A1
; GENERAL INFORMATION:
; APPLICANT: University of Rochester
; APPLICANT: Zauderer, Maurice
; APPLICANT: Ernest S. Smith
; TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
; TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells
; FILE REFERENCE: 1821.0070004
; CURRENT APPLICATION NUMBER: US/09/987,456
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/271,424
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/262,067
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/298,087
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/249,268
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 149
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p7.5/ATG2/tk vector
US-09-987-456-4

```

```

Query Match          92.6%; Score 137; DB 10; Length 149;
Best Local Similarity 99.3%; Pred. No. 6,1e-43;
Matches 148; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```

```

QY 1 GGGCAAAATTTGAAAACATGATCTATTTATTTGACAGCGGCCCATG-GTGAATCCCG 59
    |||||||
DB 1 GGGCAAAATTTGAAAACATGATCTATTTATTTGACAGCGGCCCATGAGTGAATCCCG 60
    |||||||
QY 60 GGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTTCAGCCCTCGAGGGGGCCTTA 119
    |||||||
DB 61 GGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTTCAGCCCTCGAGGGGGCCTTA 120
    |||||||
QY 120 TAATAATTTGTTTGTGGGGCCGGCC 148
    |||||||
DB 121 TAATAATTTGTTTGTGGGGCCGGCC 149
    |||||||

```

```

RESULT 5
US-09-822-250-9
; Sequence 9, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
; CURRENT APPLICATION NUMBER: US/09/822,250
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 150
; TYPE: DNA
; ORGANISM: synthetic construct

```


RESULT 7
US-09-822-250-6
; Sequence 6, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice

QY	1	GGCAGAAATTTGAAAACCTAGATCTATTPTTTCAGCGGCCGCATGGTGGATCCCGC	60
Db	1	GGCAGAAATTTGAAAACCTAGATCTATTPTTTCAGCGGCCGC---GTGATCCCCG	57
QY	61	GGCTGAGGAATTCATATTCAGAGTTTCATACCGTCGACCTCGAGGGGGGGCTAACT	120
Db	58	GGCTGAGGAATTCATATTCAGAGTTTCATACCGTCGACCTCGAGGGGGGGGGCTAACT	117

QY	121	AACTAATTTTGTGTTTGTGGCCCGGCC	148
Db	118	AACTAATTTTGTGTTTGTGGCCCGGCC	145

```

RESULT 9
US-09-735-705-91
? Sequence 91, Application US/09735705
? Patent No. US20020052329A1
? GENERAL INFORMATION:
? APPLICANT: Wang, Tongtong
? APPLICANT: Fan, Liqun
? APPLICANT: Kalos, Michael D.
? APPLICANT: Bangour, Chaitanya S.
? APPLICANT: Hosken, Nancy
? APPLICANT: Fanger, Gary R.
? APPLICANT: Li, Samuel X.
? APPLICANT: Wang, Aijun
? APPLICANT: Skeiky, Yasir A.W.
? APPLICANT: Henderson, Robert A.
? APPLICANT: McNeill, Patricia D.
? APPLICANT: Fanger, Neil
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
? TITLE OF INVENTION: AND DIAGNOSIS OF LONG CANCER
? FILE REFERENCE: 210121.455C14
? CURRENT APPLICATION NUMBER: US/09/735,705
? CURRENT FILING DATE: 2000-12-12
? NUMBER OF SEQ ID NOS: 419
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 91
? LENGTH: 858
? TYPE: DNA
? ORGANISM: Homo sapien
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1)...(858)
? US-09-735-705-91

```

```

RESULT 10
US-09-850-716A-91
; Sequence 91, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Kelter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ. ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 91
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE: 3

```

```

; NAME/KEY: misc_feature
; LOCATION: (1)...(858)
; OTHER INFORMATION: n = A,T,C or G
US-09-850-716A-91

Query Match      47.7%; Score 70.6; DB 10; Length 858;
Best Local Similarity 84.9%; Pred. No. 3.2e-17;
Matches 79; Conservative 0; Mismatches 14; Indels 0; Gaps

QY    23 TCTATTATTTGGACGCGGCCGCATGTGTGATCCCGCGGGCTGCAGAAATTCGATATCAA 82
      ||| ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db     331 TCACGAATTTCCACACACACKCTGGACTATATGGATATCCCCGGGGCTGAGAAATTCGATATCAA 390

QY    83 GCTTATCGATTACCCTTGCACTCGAAGGGGGGGGCC 115
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     391 GCTTATCGATTACCCTTGCACTCGAAGGGGGGGGCC 423
```

```

RESULT 11
US-09-897-778-91
; Sequence 91, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnierakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vegdick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 91
LENGTH: 858
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 570..591, 655, 664, 667, 683, 711, 759, 760, 765, 777, 787,
LOCATION: 792, 794, 801, 804, 809, 817, 820
OTHER INFORMATION: n = A,T,C or G
US-09-897-778-91

Query Match          47.7%; Score 70.6; DB 10; Length 858;
Best Local Similarity 84.9%; Pred. No. 3,2e-17;
Matches    79; Conservative      0; Mismatches   14; Indels       0; Gaps     0.

QY      23 TCTATTATTCACGCGGCCGCCCATGTGGATCCCGCGGGCGAGGATTCGATATCA 82
        ||| ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      331 TCACAAGAATTCACGCACACTGTGACTGTGATCCCGCGGGTGCAGGAATTCGATATCA 390
        ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      83 GCCTATCGATACCGTGACCTCGAGCGGGGGCC 115
        ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      391 GCTTATCGATACCGTCGACCTCGAGGGGGGCC 423
        ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 12
US-09-834-975-541/c
; Sequence 541, Application US/09834975
; Patent No. US20020110815A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Brown, Jeffrey
; APPLICANT: Bolt, Andrew
; APPLICANT: Van Hufel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS

```

```
; TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF HUMAN CANCERS
; FILE REFERENCE: MRI-016B
; CURRENT APPLICATION NUMBER: US/09/834,975
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,538
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 1046
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 541
; LENGTH: 574
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-975-541
```

```
Query Match          47.2%; Score 69.8; DB 10; Length 574;
Best Local Similarity 73.6%; Pred. No. 5.4e-17;
Matches 89; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
```

```
QY 13 AAAACGTAGCTATTATTCACAGCGCGCCCATGGTGATCCCGCGGCTGAGGAAT 72
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 134 AACGTTAAATTTACACCTCGCGCTCTAGAACTAGTGTGATCCCGCGGCTGAGGAAC 75
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 73 TCGATATCAACCTTATGATACCTCGACCTCGAGGGGGGCTTAACCTAATTTGT 132
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 74 TCGATATCAACCTTATGATACCTCGACCTCGAGGGGGGCTTAACCTAATTTGT 15
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 133 T 133
Db 14 T 14
```

```
RESULT 13
US-09-834-975-601/C
; Sequence 601, Application US/09834975
; Patent No. US20020110815A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Brown, Jeffrey
; APPLICANT: Bolt, Andrew
; APPLICANT: Van Hufel, Christophe
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; FILE REFERENCE: MRI-016B
; CURRENT APPLICATION NUMBER: US/09/834,975
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,538
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 1046
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 601
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-975-601
```

```
Query Match          46.9%; Score 69.4; DB 10; Length 424;
Best Local Similarity 87.4%; Pred. No. 6.6e-17;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
```

```
QY 47 TGGTGGATCCCCGGGCTGAGGAATTCGATATCAAGCTTATCGATACCGTGACCTCGA 106
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 106 TAGTGGATCCCCGGGCTGAGGAATTCGATATCAAGCTTATCGATACCGTGACCTCGA 47
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 107 GGGGGGCTTAACCTAATTTGT 133
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 46 GGGGGGCTTAACCTAATTTGT 20
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 14
US-09-784-130-9/C
; Sequence 9, Application US/09784130
```

```
; Patent No. US20020076808A1
; GENERAL INFORMATION:
; APPLICANT: Donahue, Brian A.
; APPLICANT: Hardy, Stephen F.
; APPLICANT: Snyder, Richard O.
; APPLICANT: Cell Genesys, Inc.
; TITLE OF INVENTION: USE OF SUPPRESSOR tRNA's TO REGULATE CYTOTOXICITY
; TITLE OF INVENTION: DURING THE PRODUCTION OF RECOMBINANT GENE PRODUCTS
; FILE REFERENCE: P132222
; CURRENT APPLICATION NUMBER: US/09/784,130
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/097,328
; PRIOR FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 9
; LENGTH: 118
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: polylinker
US-09-784-130-9
```

```
Query Match          45.5%; Score 67.4; DB 10; Length 118;
Best Local Similarity 98.6%; Pred. No. 2e-16;
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 47 TGGTGGATCCCCGGGCTGAGGAATTCGATATCAAGCTTATCGATACCGTGACCTCGA 106
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 93 TAGTGGATCCCCGGGCTGAGGAATTCGATATCAAGCTTATCGATACCGTGACCTCGA 34
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 107 GGGGGGCTTAACCTAATTTGT 133
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 33 GGGGGGCTTAACCTAATTTGT 25
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 15
US-09-735-705-306
; Sequence 306, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 306
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-735-705-306
```

```
Query Match          45.5%; Score 67.4; DB 10; Length 457;
Best Local Similarity 98.6%; Pred. No. 3.9e-16;
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 47 TGGTGGATCCCCGGGCTGAGGAATTCGATATCAAGCTTATCGATACCGTGACCTCGA 106
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Db 358 TAGTGATCCCCGGGCTGCAGAAATTCGATATCAAGCTATCGATACGTCGACCTCGA 417

OY 107 GGGGGGGCC 115
|||||

Db 418 GGGGGGGCC 426

Search completed: November 10, 2002, 11:33:46
Job time : 37.836 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:43:30 : Search time 37.943 Seconds
(without alignments)
1196.219 Million cell updates/sec

Title: US-08-935-377-7

Perfect score: 148

Sequence: 1 GGCCAAAATGAAAACTA.....TTGTTTGTGGGCGCCGCC 148

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCrus_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70.6	47.7	858	4	US-09-123-912-91
2	70.6	47.7	858	4	US-09-643-597-91
3	69.4	46.9	229	4	US-09-116-482A-39
4	68.4	46.2	793	2	US-08-967-101-121
5	68.4	46.2	793	2	US-08-592-541-121
6	68.4	46.2	793	3	US-09-124-698-121
7	68.4	46.2	793	4	US-09-127-480-121
8	68.4	46.2	793	4	US-08-496-841C-121
9	68.4	46.2	793	4	US-09-124-523-121
10	68	45.9	5356	4	US-08-446-935-1
11	67.4	45.5	147	4	US-09-323-872A-26
12	67.4	45.5	457	4	US-09-643-597-306
13	67.4	45.5	752	4	US-08-976-259-108
14	67.4	45.5	2961	4	US-08-446-935-6
15	67.4	45.5	3792	2	US-08-993-334-1
16	67.4	45.5	3792	2	US-08-302-752-1
17	67.4	45.5	4016	1	US-08-410-540-3
18	67.4	45.5	5234	3	US-08-993-334-2
19	67.4	45.5	5234	3	US-08-302-752-2
20	67.4	45.5	5592	4	US-09-495-797-37
21	67.4	45.5	6722	2	US-08-993-334-3
22	67.4	45.5	6722	3	US-08-302-752-3
23	67.2	45.4	545	4	US-08-991-789A-10
24	67.2	45.4	545	4	US-09-062-451-10
25	67.2	45.4	545	4	US-09-598-326-10
26	66	44.6	11233	4	US-08-980-832-27
27	65.4	44.2	9318	2	US-08-793-610-6

28	65.2	44.1	713	4	US-08-998-416-135	Sequence 135, Appl	
C	29	65	43.9	78	4	US-09-462-645C-25	Sequence 25, Appl
30	65	43.9	84	4	US-09-462-645C-26	Sequence 26, Appl	
31	65	43.9	698	4	US-08-998-416-54	Sequence 54, Appl	
C	32	65	43.9	3465	4	US-09-462-645C-9	Sequence 9, Appl1
C	33	65	43.9	3481	4	US-09-462-645C-11	Sequence 11, Appl
C	34	65	43.9	3794	4	US-09-462-645C-5	Sequence 5, Appl1
C	35	65	43.9	3810	4	US-09-462-645C-7	Sequence 7, Appl1
C	36	65	43.9	6596	4	US-09-575-602-11	Sequence 11, Appl1
37	62.8	42.4	685	1	US-08-465-388-56	Sequence 56, Appl	
38	62.8	42.4	685	1	US-08-204-675-1	Sequence 1, Appl1	
39	59.6	40.3	4164	2	US-08-660-754-1	Sequence 1, Appl1	
40	59.6	40.3	4164	2	US-08-796-364-1	Sequence 1, Appl1	
41	59.6	40.3	4164	5	PCT-US95-02520-1	Sequence 1, Appl1	
42	58.4	39.5	5178	2	US-08-474-169-2	Sequence 2, Appl1	
43	58.4	39.5	3198	4	US-08-842-306B-48	Sequence 48, Appl	
44	58.2	39.3	3198	4	US-08-838-973B-48	Sequence 48, Appl	
45	58.2	39.3	3198	4	US-08-838-973B-48	Sequence 48, Appl	

ALIGNMENTS

```
RESULT 1
US-09-123-912-91
Sequence 91, Application US/09123912A
Patent No. 6312695
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Reed, Steven G.
TITLE OR INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
FILE REFERENCE: 210121.455c1
CURRENT APPLICATION NUMBER: US/09/123,912A
PRIORITY FILING DATE: 1998-07-27
PRIORITY APPLICATION NUMBER: 09/040,802
PRIORITY FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 91
LENGTH: 858
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified_base
LOCATION: (570)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (591)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (655)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (664)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (667)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (683)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (711)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (759)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (760)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (765)
OTHER INFORMATION: Where n is a, c, g or t
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NAME/KEY: modified_base
LOCATION: (777)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (787)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (792)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (794)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (801)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (804)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (809)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (817)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (820)
OTHER INFORMATION: where n is a, c, g or t
US-09-123-912-91
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Query Match 47.7%; Score 70.6; DB 4; Length 858;
Best Local Similarity 84.9%; Pred. No. 1.8e-14;

Matches 79; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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QY 23 TCTATTATTCACGCGCCGCGCATGTGTGATCCCGGCGCTGCAGATTCGATATCAA 82
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 331 TCAACGATTCACACACACTGACTGAGTATCCCGGGGTGCAGATTCGATATCAA 390
QY 83 GCTTATCGATACCGTCGACCTCGAGGGGGGCC 115
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 391 GCTTATCGATACCGTCGACCTCGAGGGGGGCC 423
```

RESULT 2

US-09-643-597-91

; Sequence 91, Application US/09643597
; Patent No. 6426072

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kaios, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Henderson, Robert A.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.455C11

; CURRENT APPLICATION NUMBER: US/09/643,597

; CURRENT FILING DATE: 2000-08-21

; NUMBER OF SEQ ID NOS: 369

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 91

; LENGTH: 858

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(858)

; OTHER INFORMATION: n = A,T,C or G

US-09-643-597-91

Query Match 47.7%; Score 70.6; DB 4; Length 858;
Best Local Similarity 84.9%; Pred. No. 1.8e-14;

Matches 79; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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QY 23 TCTATTATTCACGCGCCGCGCATGTGTGATCCCGGCGCTGCAGATTCGATATCAA 82
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 331 TCAACGATTCACACACACTGACTGAGTATCCCGGGGTGCAGATTCGATATCAA 390
QY 83 GCTTATCGATACCGTCGACCTCGAGGGGGGCC 115
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 391 GCTTATCGATACCGTCGACCTCGAGGGGGGCC 423
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RESULT 3

US-09-116-492A-39/C

; Sequence 39, Application US/09116492A
; Patent No. 6436409

; GENERAL INFORMATION:

; APPLICANT: GICOUEL, BRIGITTE

; APPLICANT: BERTHET, FRANCOIS-XAVIER

; APPLICANT: ANDERSEN, PETER

; APPLICANT: RASMUSSEN, PETER B

; TITLE OF INVENTION: POLYNUCLEOTIDE FUNCTIONALLY CODING FOR THE LHP PROTEIN FROM MY

; TITLE OF INVENTION: TUBERCULOSIS, ITS BIOLOGICALLY ACTIVE DERIVATIVE FRAGMENTS, A

; FILE REFERENCE: 0660-0137-27X

; CURRENT APPLICATION NUMBER: US/09/116,492A

; CURRENT FILING DATE: 1998-07-16

; PRIOR APPLICATION NUMBER: 60/252,631

; PRIOR FILING DATE: 1997-07-16

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 39

; LENGTH: 229

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: multiple cloning site-artificial DNA

US-09-116-492A-39

Query Match 46.9%; Score 69.4; DB 4; Length 229;
Best Local Similarity 87.4%; Pred. No. 3.1e-14;

Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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QY 47 TGGTGAATCCCGGGGCTGAGGATTCGATATCAAGCTTATCGATACCGTCACTCGA 106
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 142 TAGTGAATCCCGGGGCTGAGGATTCGATATCAAGCTTATCGATACCGTCACTCGA 83
QY 107 GGGGGGGCCTAAGTAACTAATTTTGT 133
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 82 GGGGGGGCCTAAGTAACTAATTTTGT 56
```

RESULT 4

US-08-967-101-121/C

; Sequence 121, Application US/08967101
; Patent No. 5840540

; GENERAL INFORMATION:

; APPLICANT: ST. GEORGE-HYSLOP, PETER H

; APPLICANT: ROMERS, JOHANNA M

; APPLICANT: FRASER, PAUL E

; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED

; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE

; NUMBER OF SEQUENCES: 183

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TESTA, HURWITZ & THIBEAULT

; STREET: High Street Tower - 125 High Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-967-101-121

Query Match 46.2%; Score 68.4; DB 2; Length 793;
Best Local Similarity 87.2%; Pred. No. 9.4e-14;

Matches 75; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 48 GGTGATCCCCCGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 107

DB 119 GGGGATCCCCCGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 60

QY 108 GGGGGCCTAAGTAATTAATTTGTT 133
|||
DB 59 GGGGGCCTAAGTAATTTGTT 34

RESULT 5
US-08-592-541-121/c
Sequence 121, Application US/08592541
Patent No. 5986054
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:

LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-592-541-121

Query Match 46.2%; Score 68.4; DB 2; Length 793;
Best Local Similarity 87.2%; Pred. No. 9.4e-14;
Matches 75; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 48 GGTGATCCCCCGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 107

DB 119 GGGGATCCCCCGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 60

QY 108 GGGGGCCTAAGTAATTAATTTGTT 133
|||
DB 59 GGGGGCCTAAGTAATTTGTT 34

RESULT 6
US-09-124-698-121/c
Sequence 121, Application US/09124698
Patent No. 6117978
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,698
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-124-698-121

Query Match 46.2%; Score 68.4; DB 3; Length 793;
Best Local Similarity 87.2%; Pred. No. 9.4e-14;
Matches 75; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 48 GGTGATCCCCCGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 107

DB 119 GGGGATCCCCCGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 60

QY 108 GGGGGCCTAAGTAATTTGTT 133

Db 59 GGGGGGCCGGTACCAGCTTTGTT 34

RESULT 7

US-09-127-480-121/c
; Sequence 121, Application US/09127480
; Patent No. 6194153
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/127,480
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 793 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-127-480-121

Query Match 46.2%; Score 68.4; DB 4; Length 793;

Best Local Similarity 87.2%; Pred. No. 9.4e-14;
Matches 75; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 48 GGTGATCCCCCGGCGAGCAATTCGATATCAAGCTTATCGATACCGTCGAG 107
|||
Db 119 GCGGATCCCCCGGCGAGCAATTCGATATCAAGCTTATCGATACCGTCGAG 60

QY 108 GGGGGCCCTAAGTAATTTGTT 133
|||
Db 59 GGGGGCCCGTACCAGCTTTGTT 34

RESULT 8

US-08-496-841C-121/c
; Sequence 121, Application US/08496841C
; Patent No. 6210919
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Darby & Darby, PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/496,841C
FILING DATE: 28-Jun-1995
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Paul F. Fehner, Ph.D.

REGISTRATION NUMBER: 35,135

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237

INFORMATION FOR SEQ ID NO: 121:

SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 121:

US-08-496-841C-121

Query Match 46.2%; Score 68.4; DB 4; Length 793;

Best Local Similarity 87.2%; Pred. No. 9.4e-14;
Matches 75; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 48 GGTGATCCCCCGGCGTGCAGCAATTCGATATCAAGCTTATCGATACCGTCGAG 107
|||
Db 119 GCGGATCCCCCGGCGTGCAGCAATTCGATATCAAGCTTATCGATACCGTCGAG 60

QY 108 GGGGGCCCTAAGTAATTTGTT 133
|||
Db 59 GGGGGCCCGTACCAGCTTTGTT 34

RESULT 9

US-09-124-523-121/c
; Sequence 121, Application US/09124523
; Patent No. 6395960
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/124,523
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,541

FILED DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-124-523-121

Query Match 46.2%; Score 68.4; DB 4; Length 793;
Best Local Similarity 87.2%; Pred. No. 9.4e-14;
Matches 75; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 48 GGGGATCCCCCGGCGTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 107
|||
Db 119 GGGGATCCCCCGGCGTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 60
OY 108 GGGGGGCTTAAGTAAATTTGTT 133
|||||
Db 59 GGGGGGCGGTACCGACGCTTTGTT 34

RESULT 10
US-08-446-935-1/C
Sequence 1, Application US/08446935
Patent No. 6187991
GENERAL INFORMATION:
APPLICANT: Soeller, Walter C.
APPLICANT: Carty, Maynard D.
APPLICANT: Kreuter, David K.
TITLE OF INVENTION: TRANSGENIC ANIMAL MODELS FOR TYPE II
TITLE OF INVENTION: DIABETES MELLITUS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pfizer Inc.
STREET: 235 East 42nd Street, 20th Floor
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10017-5755
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,935
FILING DATE:

CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sheyka, Robert F.
REGISTRATION NUMBER: 31,304
REFERENCE/DOCKET NUMBER: PC8153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)573-1189
TELEFAX: (212)573-1939
TELEX: N/A
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5356 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
US-08-446-935-1

Query Match 45.9%; Score 68; DB 4; Length 5356;

Best Local Similarity 88.1%; Pred. No. 2.2e-13;
Matches 74; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 32 TGCACGGGCCCCCATGTGATCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGA 91
| | | | |
Db 743 TCCACTTGGAGTGTGGGGGATCCCGGCTGCAGAAATTCGATATCAAGCTTATCGA 684
OY 92 TACCGTCGACCTCGAGGGGGGCC 115
|||||
Db 683 TACCGTCGACCTCGAGGGGGGCC 660

RESULT 11
US-09-323-872A-26/C
Sequence 26, Application US/09323872A
Patent No. 6395359
GENERAL INFORMATION:
APPLICANT: Coschigano, Peter
TITLE OF INVENTION: Compositions and Methods for Bioremediation
FILE REFERENCE: OHU-03640
CURRENT APPLICATION NUMBER: US/09/323,872A
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 09/072,433
PRIOR FILING DATE: 1998-05-04
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin version 3.0
SEQ ID NO 26
TYPE: DNA
LENGTH: 147
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(147)
US-09-323-872A-26

Query Match 45.5%; Score 67.4; DB 4; Length 147;
Best Local Similarity 98.6%; Pred. No. 1.3e-13;
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 47 TGTGTGATCCCCCGGCGTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 106
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Db 108 TAGTGTGATCCCCCGGCGTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 49
OY 107 GGGGGGGGCC 115
|||||
Db 48 GGGGGGGGCC 40

RESULT 12
US-09-643-597-306
Sequence 306, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSeq for Windows version 3.0
SEQ ID NO 306
LENGTH: 457


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1 COUNTRY: United States
2
3 ZIP: 91105
4
5 COMPUTER READABLE FORM:
6
7 MEDIUM TYPE: floppy disk
8
9 COMPUTER: IBM PC compatible
10
11 OPERATING SYSTEM: PC-DOS/MS-DOS
12
13 SOFTWARE: Patent In Release #1.0, V
14
15 CURRENT APPLICATION DATA:
16
17 APPLICATION NUMBER: US/08/992,334
18
19 FILING DATE: 17-DEC-1997
20
21 CLASSIFICATION: 435
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23 PRIOR APPLICATION DATA:
24
25 APPLICATION NUMBER:
26
27 FILING DATE: 24-DEC-1994
28
29 PRIOR APPLICATION DATA:
30
31 APPLICATION NUMBER: PCT/FR93/00248
32
33 FILING DATE: 12-MAR-1993
34
35 PRIOR APPLICATION DATA:
36
37 APPLICATION NUMBER: FR 9R92/03034
38
39 FILING DATE: 13-MAR-1992
40
41 ATTORNEY/AGENT INFORMATION:
42
43 NAME: Prout, D. Bruce
44
45 REGISTRATION NUMBER: 20958
46
47 REFERENCE/DOCKET NUMBER: C93:31779
48
49 TELECOMMUNICATION INFORMATION:
50
51 TELEPHONE: (626) 795-9500
52
53 TELEFAX: (626) 577-8800
54
55 INFORMATION FOR SEQ ID NO: 1:
56
57 SEQUENCE CHARACTERISTICS:
58
59 LENGTH: 3792 base pairs
60
61 TYPE: nucleic acid
62
63 STRANDEDNESS: both
64
65 TOPOLOGY: circular
66
67 MOLECULE TYPE: DNA (genomic)
68
69 HYPOTHEetical: NO
70
71 ANTI-SENSE: YES
72
73 IMMEDIATE SOURCE:
74
75 CLONE: pc+host4
76
77 US-08-992-334-1

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:05:45 ; Search time 724.448 Seconds

(without alignments)
5985.683 Million cell updates/sec

Title: US-08-935-377-8

Perfect score: 149
Sequence: 1 GCCCAAAATGAAAACTA.....TTGTTTGTGCGCCGCC 149

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: gb_hcg:*
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6: gb_pat:*
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16: em_fun:*
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35: em_htg_rod:*
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41: em_hlgo_other:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	149	100.0	149	6 AX326745	AX326745 Sequence
2	138	92.6	150	6 AX326746	AX326746 Sequence
3	137	91.9	148	6 AX326744	AX326744 Sequence
4	131	87.9	145	6 AX326743	AX326743 Sequence
5	73.6	49.4	5639	12 CV014122	U14122 Cloning vec
6	71.2	47.8	259	6 A44281	A44281 Sequence 9
7	70.8	47.5	859	11 CNE06EDT	AL394983 T7 end of
8	70.4	47.2	525	5 AF309793	AF309793 Clupea pa
9	70.2	47.1	13558	6 AX287041	AX287041 Sequence
10	70	47.0	424	6 AX284796	AX284796 Sequence
11	70	47.0	2059	12 AT034154	AT034154 Cloning v
12	70	47.0	2850	9 AB035274	AB035274 Homo sap1
13	70	47.0	2958	6 AX247548	AX247548 Sequence
14	70	47.0	2958	12 ARBLKSM	X52326 pbuescript
15	70	47.0	2958	12 ARBLKSP	X52329 pbuescript
16	70	47.0	2961	12 ARBL2KSM	X52327 pbuescript
17	70	47.0	2961	12 ARBL2KSP	X52327 pbuescript
18	70	47.0	2964	12 SYNBLSKSV	L08784 Bluescribe
19	70	47.0	2964	12 SYNBLSKSPV	L08784 Bluescribe
20	70	47.0	3306	12 SYNBBEN66	DB5525 Cloning vec
21	70	47.0	3417	12 AF153422	AF153422 Cloning v
22	70	47.0	3485	12 AF178449	AF178449 Integrati
23	70	47.0	4144	12 XX035131	U35131 Plasmid pbs
24	70	47.0	4267	12 PRS304	U35136 Plasmid pbs
25	70	47.0	4289	12 PRS306	U35136 Plasmid pbs
26	70	47.0	4373	12 PRS303	U03438 yeast integ
27	70	47.0	4443	12 PRS303	U03435 yeast integ
28	70	47.0	4549	12 AF178452	AF178452 Integrati
29	70	47.0	4670	12 ASAJ5326	AJ005326 pgAT1(+)
30	70	47.0	4670	12 ASAJ5329	AJ005329 pgAT1(-)
31	70	47.0	4707	12 XX023774	U02374 Cloning vec
32	70	47.0	4768	12 XX025061	U25061 Cloning vec
33	70	47.0	4783	12 PRS314	U03440 yeast centr
34	70	47.0	4887	12 PRS316	U03442 yeast centr
35	70	47.0	4950	12 XX025060	U25060 Cloning vec
36	70	47.0	4967	12 PRS313	U03439 yeast centr
37	70	47.0	5144	12 CV023751	U23751 Cloning vec
38	70	47.0	5187	12 U34887	U34887 yeast integ
39	70	47.0	5228	12 XX025059	U25059 Cloning vec
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41	70	47.0	5634	12 CV014125	U14125 Cloning vec
42	70	47.0	5973	12 AF504908	AF504908 Cloning v
43	70	47.0	6018	12 PRS315	U03441 yeast centr
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45	70	47.0	9655	12 SYNPCR8V	AD001531 Cloning v

ALIGNMENTS

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RESULT 1
AX326745 LOCUS AX326745 149 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 6 from Patent WO0172995.
ACCESSION AX326745
VERSION AX326745.1 GI:18097471
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
REFERENCE
1 Zauderer,M. and Smith,E.S.
METHODS OF PRODUCING A LIBRARY AND METHODS OF SELECTING
POLYNUCLEOTIDES OF INTEREST
Patent: WO 0172995-A 6 04-OCT-2001;
JOURNAL
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UNIVERSITY OF ROCHESTER (US)									
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source	1..149								
	/organism="synthetic construct"								
	/db_xref="taxon:32630"								
	/note="Nucleotide Sequence of p7.5/AmG2/Lk"								
BASE COUNT	36 a 37 c 39 g 37 t								
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Query Match	100.0%; Score 149; DB 6; Length 149;								
Best Local Similarity	100.0%; Pred. No. 4e-35;								
Matches 149; Conservative	0; Mismatches 0; Indels 0; Gaps 0;								
OY	1 GGGCCAAAATGAAAACTAGATCTATTATTATGACGGCGCCGCCCATGATGATCCCC 60								
DB	1 GGGCCAAAATGAAAACTAGATCTATTATTATGACGGCGCCGCCCATGATGATCCCC 60								
OY	61 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTTCGAGGGGGGCGCTAAC 120								
DB	61 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTTCGAGGGGGGCGCTAAC 120								
OY	121 TTACTAATTTGTTGTTTGGGGCCCGGGCC 149								
DB	121 TTACTAATTTGTTGTTTGGGGCCCGGGCC 149								
RESULT 2									
LOCUS	AX326746 150 bp DNA linear PAT 07-JAN-2002								
DEFINITION	Sequence 7 from Patent W00172955.								
ACCESSION	AX326746								
VERSION	AX326746.1 GI:18097472								
KEYWORDS	synthetic construct.								
SOURCE	synthetic construct								
ORGANISM	artificial sequences.								
REFERENCE	1								
AUTHORS	Zauderer,M. and Smith,E.S.								
TITLE	Methods of producing a library and methods of selecting								
JOURNAL	polynucleotides of interest								
	Patent: WO 017295-A 7 04-OCT-2001;								
FEATURES	UNIVERSITY OF ROCHESTER (US)								
source	Location/Qualifiers								
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Matches 149; Conservative	0; Mismatches 0; Indels 1; Gaps 1;								
OY	1 GGGCCAAAATGAAAACTAGATCTATTATTATGACGGCGCCGCCATGA-GTGGATCCCC 59								
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OY	60 CGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTTCGAGGGGGGCGCTAA 119								
DB	61 CGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTTCGAGGGGGGCGCTAA 120								
OY	120 CTAAGTAATTTGTTTGGGGCCCGGCC 149								
DB	121 CTAAGTAATTTGTTTGGGGCCCGGCC 150								
RESULT 3									
LOCUS	AX326744 148 bp DNA linear PAT 07-JAN-2002								
DEFINITION	Sequence 5 from Patent W00172955.								
ACCESSION	AX326744								
VERSION	AX326744.1 GI:18097470								

[illegible]

REFERENCE	PUBMED	11152876
AUTHORS	2 (bases 1 to 859)	
TITLE	de Montigny,J., Straub,M., Potier,S., Tekala,F., Dujon,B., Wincker,P., Artiguenave,F. and Souciet,J.	
JOURNAL	Genomic exploration of the hemiascomycetous yeasts: 8.	
MEDLINE	Zygosaccharomyces rouxii	
PUBMED	FEBS Lett. 487 (1), 52-55 (2000)	
REFERENCE	20584718	
AUTHORS	11152883	
TITLE	3 (bases 1 to 859)	
JOURNAL	Genoscope.	
COMMENT	Direct Submission Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seque@genoscope.cns.fr - Web : www.genoscope.cns.fr) This SFS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert. Location/Qualifiers	
FEATURES	source	1..859
	/organism="Zygosaccharomyces rouxii"	
	/strain="CBS 732"	
	/db_xref="taxon:4956"	
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	/clone_lib="FAR0A"	
	/note="End : T7"	
STS	1..859	
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Best Local Similarity	79.2%	Pred. No. 4.9e-11;
Matches	84; Conservative 0; Mismatches 22; Indels 0; Gaps 0;	
OY	11 TGAAGACTAGATCTATTATTCACGCGCGCCCATGATGATCCCGGGCTGCAGG 70	
DB	730 TGAAGAAATACGCTATTCTTTCATCAAGAGTCCACAGTATATGATGCCCGGGCTGCAGG 789	
OY	71 AATTGATATCAAGCTTATCGATTACCGTGCAGCTCGAGGGGGGCC 116	
DB	790 AATTGATATCAAGCTTATCGATTACCGTGCAGCTCGAGGGGGGCC 835	
RESULT 8		
LOCUS	AF309793	525 bp DNA linear VRT 23-JAN-2002
DEFINITION	Clupea pallasi microsatellite Chai13 sequence.	
VERSION	AF309793	
KEYWORDS	AF309793.1 GI:12060921	
SOURCE		
ORGANISM	Clupea pallasi.	
	Clupea pallasi.	
	Euharoptera; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae; Clupea.	
REFERENCE	1 (bases 1 to 525)	
AUTHORS	Miller,K.M., Laboree,K., Schulze,A.D. and Kaukinen,K.H.	
TITLE	Development of microsatellite loci in Pacific herring (Clupea pallasi)	
JOURNAL	Mol. Ecol. Notes 1 (3), 131-132 (2001)	
REFERENCE	2 (bases 1 to 525)	
AUTHORS	Miller,K.M., Laboree,K. and Kaukinen,K.	
TITLE	Direct Submission	
JOURNAL	Submitted (02-OCT-2000) Aquaculture/Genetics, Pacific Biological Station, Hammond Bay Rd., Nainaimo, B.C. V9R 5K6, Canada	
FEATURES	Location/Qualifiers	

source	1. .525	/organism="Clupea pallasi"
	/db_xref="taxon:30724"	
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repeat_region	1. .525	/note="microsatellite Chall3"
	/rpl_type=randem	
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Query Match	47.2%; Score 70.4; DB 5; Length 525;	
Best Local Similarity	79.8%; Pred. No. 6e-11;	
Matches	83; Conservative 0; Mismatches 21; Indels 0; Gaps 0;	
Qy	31 TTGCACGGGCGCCGATGATGATGATCCCCCGGGCTGCAGGAATTGCATATCAAGCTATAC 90	
DB	126 TTGCATGAGAGACACCCGACACAGATCCCCCGGGCTGCAGGAATTGCATATCAAGCTATAC 67	
Qy	91 GATACCGTCGACCTCGAGGGGGGCTTAACCTAATATTTGTT 134	
DB	66 GATACCGTCGACCTCGAGGGGGGCTTAACCTAATATTTGTT 23	
RESULT 9		
LOCUS	AX287041 13558 bp DNA linear PAT 21-NOV-2001	
DEFINITION	Sequence 5 from Patent WO0181623.	
ACCESSION	AX287041	
VERSION	AX287041.1 GI:17049037	
KEYWORDS		
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
TITLE	1 Goetzl B., Kammandel B., Kuner R., Scheek S. and Hiesmisch H.	
JOURNAL	Novel neuronally expressed protein and use thereof	
FEATURES	Patent: WO 0181623-A 5 01-NOV-2001;	
source	Location/Qualifiers	
	1. .13558	
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ORIGIN		
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Best Local Similarity	96.0%; Pred. No. 1.1e-10;	
Matches	72; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
Qy	42 CGCCATGATGATGATCCCCGGGCTGCAGGAATTGCATATCAAGCTTATCGATACCGTCGA 101	
DB	13479 CGCAAGGCGTGATCCCCCGGGCTGCAGGAATTGCATATCAAGCTTATCGATACCGTCGA 13558	
Qy	102 CCTCGAGGGGGGGCC 116	
DB	13539 CCTCGAGGGGGGGCC 13553	
RESULT 10		
LOCUS	AX284796/c 424 bp DNA linear PAT 20-NOV-2001	
DEFINITION	AX284796 Sequence 601 from Patent WO0179556.	
ACCESSION	AX284796	
VERSION	AX284796.1 GI:17045484	
KEYWORDS		
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE	1 Little J., Brown J.L., Bolt A. and van Hufel C.	
	Novel genes, compositions and methods for the identification,	

Assessment, prevention, and therapy of human cancers
JOURNAL Patent: WO 0179556-A 601 25-OCT-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES
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Best Local Similarity 88.4%; Pred. No. 7.8e-11;
Matches 76; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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DB 105 AGTGCATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 46
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QY 109 GGGGGCCCTAAGTAACTAATTTGTT 134
|||||
DB 45 GGGGGCCCGGTACCCAGCTTTGTT 20
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AY034154 2059 bp DNA circular SYN 23-JUL-2001
LOCUS Cloning vector PIDM4, complete sequence.
ACCESSION AY034154
VERSION AY034154.1 GI:14324126
KEYWORDS Cloning vector PIDM4.
SOURCE Cloning vector PIDM4
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 2059)
AUTHORS Hamilton,H.L., Schwartz,K.J. and Dillard,J.P.
TITLE Insertion-duplication mutagenesis of neisseria: use in
characterization of DNA transfer genes in the gonococcal genetic
island
JOURNAL J. Bacteriol. 183 (16), 4718-4726 (2001)
MEDLINE 21359313
PIRBASE 11466274
2 (bases 1 to 2059)
AUTHORS Hamilton,H.L., Schwartz,K.J. and Dillard,J.P.
TITLE Direct Submission
JOURNAL Submitted (11-MAY-2001) Medical Microbiology & Immunology,
University of Wisconsin-Madison, 1300 University Avenue, Madison,
WI 53706, USA
FEATURES
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complement(187..204)
/note="T7"
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RBS

-10-signal complement(1086..1091)
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-35-signal
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1130..1139
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complement(1145..1154)
/note="DNA uptake sequence (DUS)"
complement(1276..1976)
/note="RNA II"
misc_RNA
complement(1422..1423)
rep_origin
-35-signal 1830..1835
-10-signal 1854..1859
misc_RNA 1866..1973
/note="RNA I"
complement(1984..1989)
-35-signal complement(2007..2012)
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Best Local Similarity 88.4%; Pred. No. 9.9e-11;
Matches 76; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 49 AGTGCATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
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DB 144 AGTGCATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 85
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QY 109 GGGGGCCCTAAGTAACTAATTTGTT 134
|||||
DB 84 GGGGGCCCGGTACCCAGCTTTGTT 59
RESULT 12
AB035274 2890 bp mRNA linear PRI 12-JUL-2000
LOCUS Homo sapiens mRNA for postreplication repair protein hRAD18p,
DEFINITION complete cds.
ACCESSION AB035274
VERSION AB035274.1 GI:8980616
KEYWORDS
SOURCE
ORGANISM Homo sapiens placenta cDNA to mRNA.
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
TITLE 1 (sites)
AUTHORS Tateishi,S., Sakuraba,Y., Masuyama,S., Inoue,H. and Yamazumi,M.
TITLE repair and hypersensitivity to multiple mutagens
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7927-7932 (2000)
MEDLINE 20345089
2 (bases 1 to 2890)
AUTHORS Tateishi,S., Yamazumi,M. and Inoue,H.
TITLE Direct Submission
JOURNAL Submitted (26-NOV-1999) Satoshi Tateishi, Kumamoto University,
Institute of Molecular Embryology, Kujohji 4-24-1, Kumamoto,
Kumamoto 862-0976, Japan (E-mail:tateigpo.kumamoto-u.ac.jp,
tel:81-096-373-6602, Fax:81-096-373-6604)
FEATURES
source Location/Qualifiers
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/chromosome="3"
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126..1613
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KEASPAATKETRESVEELIADPSEAKREPESTLAKCVTVDCPVCGVNPESHNK
HDSCLSPREEKESLSVHKRKPLPKTVYMLSDRLKRLKEHLSIQGNKOOLIK
RHOEFVHWYNAOCALHPKSAEIVQELIENTEKTMRLEAKLNEVWVFKDOTEKE
IDELISKYRKHKRSFQOLVPOARKGYKKGMSQKTVITRKEDESTERKSSVOMGOE
DMTISVTNHSOSKLDSPDEELEPREDEESSCIDQOEVLLSSSESQSSSSDILRLD
LEEFEAWASHKNDQDTEISPRONRRTRRAESAEIPEPRKNNR"

BASE COUNT      916 a      585 c      601 g      788 t

Query Match      47.0%; Score 70; DB 9; Length 2890;
Best Local Similarity 88.4%; Pred. No. 1e-10;
Matches 76; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 49 AGTGATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
|||||
Db 2741 AGTGATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 2800
|||||

QY 109 GGGGGGCTTACTAATAATTTGTT 134
|||||
Db 2801 GGGGGGCTTACTAATAATTTGTT 2826
|||||

RESULT 13
AX247548      2958 bp      DNA      linear      PAT 28-SEP-2001
LOCUS
DEFINITION Sequence 1 from Patent WO0166775.
ACCESSION AX247548
VERSION AX247548.1 GI:15862240
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 2958)
AUTHORS Evans,D.H., Willer,D.O. and Yao,X.D.
TITLE Dna joining method
JOURNAL Patent: WO 0166775-A 1 13-SEP-2001;
          University of Guelph (CA)
FEATURES
    source
        location/Qualifiers
            1..2958
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /note="pDM101"

BASE COUNT      748 a      735 c      752 g      723 t

Query Match      47.0%; Score 70; DB 6; Length 2958;
Best Local Similarity 88.4%; Pred. No. 1e-10;
Matches 76; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 49 AGTGATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
|||||
Db 683 AGTGATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 742
|||||

QY 109 GGGGGGCTTACTAATAATTTGTT 134
|||||
Db 743 GGGGGGCTTACTAATAATTTGTT 768
|||||

RESULT 14
ARBLKSM      2958 bp      DNA      circular SYN 29-JAN-2002
LOCUS
DEFINITION pluescript KS(-) vector DNA, phagemid excised from lambda ZAP.
ACCESSION X52326
VERSION X52326.1 GI:58064
KEYWORDS artificial sequence; cloning vector; expression vector; vector.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Short,J.M., Fernandez,J.M., Sorge,J.A. and Huse,W.D.

```

```

TITLE Lambda ZAP: a bacteriophage lambda expression vector with in vivo
JOURNAL excision properties
MEDLINE Nucleic Acids Res. 16 (15), 7583-7600 (1988)
PUBMED 88319944
PUBMED 2970625
REFERENCE 2
AUTHORS Alting-Mees,M.A. and Short,J.M.
TITLE pluescript II: gene mapping vectors
JOURNAL Nucleic Acids Res. 17 (22), 9494 (1989)
MEDLINE 90067967
PUBMED 2357794
REFERENCE 3
AUTHORS Thomas,E.A.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-1990) Thomas E.A., Stratagene Clonin Systems,
11099 North Torrey Pines Rd., La Jolla, CA 92037, USA
FEATURES
    source
        1..2958
        location/Qualifiers
            1..2958
            /organism="synthetic construct"
            /db_xref="taxon:32630"
        misc_feature
            1..2958
            /note="phagemid pluescript KS(-)"

BASE COUNT      708 a      754 c      731 g      765 t

Query Match      47.0%; Score 70; DB 12; Length 2958;
Best Local Similarity 88.4%; Pred. No. 1e-10;
Matches 76; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 49 AGTGATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
|||||
Db 686 AGTGATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 745
|||||

QY 109 GGGGGGCTTACTAATAATTTGTT 134
|||||
Db 746 GGGGGGCTTACTAATAATTTGTT 771
|||||

RESULT 15
ARBLKSP      2958 bp      DNA      circular SYN 29-JAN-2002
LOCUS
DEFINITION pluescript KS(+) vector DNA, phagemid excised from lambda ZAP.
ACCESSION X52331
VERSION X52331.1 GI:58065
KEYWORDS artificial sequence; cloning vector; expression vector; vector.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Short,J.M., Fernandez,J.M., Sorge,J.A. and Huse,W.D.
TITLE Lambda ZAP: a bacteriophage lambda expression vector with in vivo
excision properties
JOURNAL Nucleic Acids Res. 16 (15), 7583-7600 (1988)
MEDLINE 88319944
PUBMED 2970625
REFERENCE 2
AUTHORS Alting-Mees,M.A. and Short,J.M.
TITLE pluescript II: gene mapping vectors
JOURNAL Nucleic Acids Res. 17 (22), 9494 (1989)
MEDLINE 90067967
PUBMED 2357794
REFERENCE 3
AUTHORS Lampe,D.J., Grant,T.E. and Robertson,H.M.
TITLE Factors affecting transposition of the Himarl mariner transposon in
vitro
JOURNAL Nucleic Acids Res. 17 (1), 179-187 (1989)
MEDLINE 98250682
PUBMED 9584095
REFERENCE 4
AUTHORS Thomas,E.A.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-1990) Thomas E.A., Stratagene Clonin Systems,
11099 North Torrey Pines Rd., La Jolla, CA 92037, USA

```

```

FEATURES             Location/Qualifiers
    source            1..2958
                        /organism="synthetic construct"
                        /db_xref="taxon:32630"
    misc_feature      1..2958
                        /note="phagemid pBluescript KS(+)"
BASE COUNT          749 a      734 c      751 g      724 t
ORIGIN

```

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Query Match          47.0%; Score 70; DB 12; Length 2958;
Best Local Similarity 88.4%; Pred. No. 1e-10; C
Matches 76; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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QY  49  AGTGGATCCCCCGGGCTCGAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
      |||||||
DB  686  AGTGGATCCCCCGGGCTCGAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 745
      |||||||
QY  109  GGGGGGCTTAACCTAATTTGTT 134
      |||||||
DB  746  GGGGGGCTTAACCTAATTTGTT 771
      |||||||

```

Search completed: November 10, 2002, 06:53:02
 Job time : 730.448 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:42:15 ; Search time 1341 Seconds

(without alignments)
1799.499 Million cell updates/sec

Title: US-08-935-377-8

Perfect score: 149
Sequence: 1 GCCCAAAATGAAAACTA.....TTGTTTGTGCGCCCGGCC 149

Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlmu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hcc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hcc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estlun:*
16: em_estlun:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76.4	51.3	891 14	BQ140386	BQ140386 NF035A10P
2	73	49.0	182 13	BI306115	BI306115 NL_3_G09
3	73	49.0	793 14	BQ143916	BQ143916 NF038H04D
4	71	47.7	682 17	AQ074693	AQ074693 CIT-HSP-2
5	70.8	47.5	804 14	BQ158468	BQ158468 NF058H09P
6	70.4	47.2	128 17	CNS07GJ4	AL609826 Anopheles

C 7	70.4	47.2	182 13	BI305962	BI305962 NL_2_K23
C 8	70.4	47.2	186 13	BI305695	BI305695 NL_1_G23
C 9	70	47.0	162 10	BE428068	BE428068 MTDO02.H1
C 10	70	47.0	390 9	AU234451	AU234451 AU234451
C 11	70	47.0	400 9	AU278852	AU278852 AU278852
C 12	70	47.0	864 17	AQ937400	AQ937400 NB2-011.H
C 13	69.8	46.8	175 13	BI306167	BI306167 NL_3_J08
C 14	69.8	46.8	182 13	BI306149	BI306149 NL_3_J07
C 15	69.8	46.8	182 13	BI306159	BI306159 NL_3_K22
C 16	69.8	46.8	182 13	BI306178	BI306178 NL_3_K05
C 17	69.8	46.8	182 13	BI306180	BI306180 NL_3_K07
C 18	69.8	46.8	175 13	BI0155148	BI0155148 NF076G11I
C 19	69.2	46.4	727 10	AM682573	AM682573 EST01439
C 20	69.2	46.4	912 17	CNS06005	AL415767 T7 end of
C 21	69.2	46.3	295 10	BE428455	BE428455 MTDO07.C0
C 22	68.6	46.0	608 17	AQ009167	AQ009167 CIT-HSP-2
C 23	68.6	46.0	212 17	CNS060D1G	AL339854 T7 end of
C 24	68.6	46.0	828 17	AQ937397	AQ937397 NB2-006.H
C 25	68.4	45.9	528 17	B63688	B63688 CIT978SK-A-
C 26	68.2	45.8	207 17	CNS060DNG	AL394034 T7 end of
C 27	68.2	45.8	728 10	AM682547	AM682547 EST01410
C 28	68	45.6	107 13	BM398556	BM398556 5009-0-47
C 29	68	45.6	108 10	BE492551	BE492551 MHE0554.C
C 30	68	45.6	108 17	B54292	B54292 CIT-HSP-201
C 31	68	45.6	124 10	AM914179	AM914179 EST345483
C 32	68	45.6	141 9	AU037147	AU037147 AU037147
C 33	68	45.6	141 17	B95279	B95279 CIT-HSP-217
C 34	68	45.6	144 17	B80294	B80294 CIT-HSP-204
C 35	68	45.6	157 12	BF281431	BF281431 EST446022
C 36	68	45.6	169 13	BI306719	BI306719 NL_5_N23
C 37	68	45.6	169 17	AQ013255	AQ013255 CIT-HSP-2
C 38	68	45.6	175 17	AQ041198	AQ041198 CIT-HSP-2
C 39	68	45.6	180 13	BI306345	BI306345 NL_4_E10
C 40	68	45.6	181 13	BI305488	BI305488 NL_0_B05
C 41	68	45.6	181 13	BI305783	BI305783 NL_1_L10
C 42	68	45.6	182 13	BI305555	BI305555 NL_0_J13
C 43	68	45.6	184 13	BI305662	BI305662 NL_1_E24
C 44	68	45.6	184 13	BI305671	BI305671 NL_1_F13
C 45	68	45.6	208 14	BM730642	BM730642 1h47d11.x

ALIGNMENTS

RESULT 1
BQ140386
LOCUS
DEFINITION
NF035A10PH1081 Phoma-infected Medicago truncatula cDNA clone
ACCESSION
BQ140386
VERSION
BQ140386.1 GI:20276512
KEYWORDS
EST.
ORGANISM
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales;
Medicago.

REFERENCE
1 (bases 1 to 891)
Watson,B.S., Shin,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R.,
Gonzales,R.A., Bell,C.J., Imman,J.T., Waugh,M.E., Sullivan,J.P.,
May,G.D. and Palva,N.L.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula Phoma-infected library
Unpublished (2002)
CONTACT: Palva NL
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7317
Fax: 580 221 7380
Email: nlpalva@noble.org
Insert Length: 891 Std Error: 0.00

JOURNAL
COMMENT

Plate: 035 row: A column: 10
Seq primer: TCACACAGGAACAGCATATGAC.

FEATURES

Location/Qualifiers
1. .891

/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF035A10PH"
/clone_lib="Phoma-infected"
/tissue_type="leaf"
/dev_stage="Pathogen-induced, young trifoliolate"

/note="Vector: Bluescript SK(-); Young trifoliolate leaves of Medicago truncatula were excised and dip-inoculated in a spore suspension of Phoma medicaginis, and inoculated in humid dishes. Pools of leaves were harvested at 0, 15, and 30 minutes and 1, 2, 3, 6, 14, 24, 48, 72, and 96, hours, and used to prepare total RNA. cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directionally ligated into the uni-zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-ZAP XR vector using Exassist helper phage and the E. coli strain XL1-Blue MRP (Stratagene). Excised plasmids were plated using SOBR cells."

BASE COUNT 188 a 151 c 64 g 224 t 264 others
ORIGIN

Query Match 51.3%; Score 76.4; DB 14; Length 891;
Best Local Similarity 87.9%; Pred. No. 2.7e-15;
Matches 80; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 49 AGTGGATCCCCGGGCTGCAGAAATTCGATTCAGCTTATCGATTACCGCTCGAG 108
|||||
Db 83 AGTGATCCCCCGGCTGCAGAAATTCGATTCAGCTTATCGATTACCGCTCGAG 142

QY 109 GGGGGCCCTAATACTATTTTGTTCGT 139
|||||
Db 143 GGGGGCCCGTANCTATTTTNCATATT 173

RESULT 2

BI306115/c 182 bp mRNA linear EST 20-JUL-2001
LOCUS NL_3_G09 Drought stress (leaf) Oryza sativa cDNA clone NL_3_G09 3',
DEFINITION mRNA sequence.

ACCESSION BI306115
VERSION BI306115.1 GI:14981437
KEYWORDS EST.

SOURCE Oryza sativa.
ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

1 (bases 1 to 182)
Reddy,A.R., Ramakrishna,W., Chandrasekhar,A., Nagabushan,I.,
Ravindrababu,P. and Bennetzen,J.L.

Novel EST enrichment with normalized cDNA libraries from drought
stressed rice (Oryza sativa L.cv Nagina 22)

JOURNAL

COMMENT

Unpublished (2001)
Contact: Reddy AR
Department of Plant Sciences, School of Life Sciences
University of Hyderabad
P.O. Central University, Hyderabad-500 046, A.P., India
Tel: 0091-40-3010265
Fax: 0091-40-3010145

Email: arjuls@uohyd.ernet.in
Insert Length: 182 Std Error: 0.00
Plate: 3 row: G column: 09

Seq primer: GTAAACGACGCCACATG.
Location/Qualifiers
1. .182

FEATURES

source
/organism="Oryza sativa"

/cultivar="Nagina 22 (indica sub sp)"

/db_xref="taxon:4530"

/clone="NL_3_G09"

/clone_lib="Drought stress (leaf)"

/tissue_type="Entire leaf tissue"

/dev_stage="35 day-old seedlings"

/note="Organ: leaf; Vector: T7T3Pac; ESTs from normalized
leaf cDNA library from drought stressed seedlings"

BASE COUNT 34 a 47 c 53 g 48 t
ORIGIN

Query Match 49.0%; Score 73; DB 13; Length 182;
Best Local Similarity 93.8%; Pred. No. 3.4e-14;
Matches 76; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 49 AGTGATCCCCCGGCTGCAGAAATTCGATTCAGCTTATCGATTACCGCTCGAG 108
|||||
Db 108 AGTGATCCCCCGGCTGCAGAAATTCGATTCAGCTTATCGATTACCGCTCGAG 49

QY 109 GGGGGCCCTAATACTATTT 129
|||||
Db 48 GGGGGCCGAGTACCAATT 28

RESULT 3

BI0143916 793 bp mRNA linear EST 24-APR-2002
LOCUS NF038H04D1F1041 Drought Medicago truncatula cDNA clone NF038H04D
DEFINITION 5', mRNA sequence.

ACCESSION BI0143916
VERSION BI0143916.1 GI:20280975
KEYWORDS EST.

SOURCE barrel medic.
ORGANISM Medicago truncatula

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabiales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.

1 (bases 1 to 793)

Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,

Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.

Expressed Sequence tags from the Samuel Roberts Noble Foundation

Medicago truncatula drought library

Unpublished (2000)

Contact: May GD

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 221 7391

Fax: 580 221 7380

Email: gdmay@noble.org

Insert Length: 793 Std Error: 0.00

Plate: 038 row: H column: 04

Seq primer: TCACACAGGAACAGCATATGAC.

Location/Qualifiers

FEATURES

source

/organism="Medicago truncatula"

/db_xref="taxon:3880"

/clone="NF038H04D"

/clone_lib="Drought"

/tissue_type="Plantlets"

/dev_stage="Pooled timepoints"

/note="Vector: Lambda zap; Contains a mixture of entire
plantlets harvested in a series of days-post-watering
timepoints."

BASE COUNT 217 a 203 c 205 g 168 t
ORIGIN

Query Match 49.0%; Score 73; DB 14; Length 793;
Best Local Similarity 93.8%; Pred. No. 3.9e-14;
Matches 76; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 49 AGTGATCCCCCGGCTGCAGAAATTCGATTCAGCTTATCGATTACCGCTCGAG 108

Db	84	AGTGGATCCCCGGGCTGCGAGGATTCGATATCAACGCTTATCGATACCTCGACCTCGAG	143
QY	109	GGGGGCGCTACTACTAATT	129
Db	144	GGGGGCGCCGAGTACCAATT	164
RESULT 4			
LOCUS	AO074693/c	682 bp	DNA
DEFINITION	CIT-HSP-2301L23.7F CIT-HSP Homo sapiens genomic clone 2301L23, DNA sequence.		
ACCESSION	AO074693		
VERSION	AO074693.1	GI:3436811	
KEYWORDS	GSS.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.		
TITLE	Use of a random human BAC End Sequence Database for Sequence-Ready Map Building		
JOURNAL	Unpublished (1998)		
COMMENT	Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html . Seq primer: M13-21 Class: BAC ends.		
FEATURES	Location/Qualifiers		
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	/db_xref="taxon:9606"		
	/clone="2301L23"		
	/clone_1lb="CIT-HSP"		
	/sex="Male"		
	/cell_type="Sperm"		
	/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII"		
BASE COUNT	156 a	187 c	187 g 151 t 1 others
ORIGIN			
Query Match	47.7%	Score 71;	DB 17; Length 682;
Best Local Similarity	93.7%;	Pred. No. 1.9e-13;	
Matches	74; Conservative	0; Mismatches	5; Indels 0; Gaps 0;
QY	49	AGTGGATCCCCGGGCTGCGAGGATTCGATATCAACGCTTATCGATACCGTCGACCTCGAG	108
Db	79	AGTGGATCCCCGGGCTGCGAGGATTCGATATCAACGCTTATCGATACCGTCGACCTCGAG	20
QY	109	GGGGGCGCTACTACTAATA	127
Db	19	GGGGGCGCCGAGTACCA	1
RESULT 5			
LOCUS	BQ158468	804 bp	mRNA
DEFINITION	NF058H09P1.F1078 Phosphate starved Leaf Medicago truncatula cDNA		
ACCESSION	BQ158468		
VERSION	BQ158468.1	GI:20295525	
KEYWORDS	EST.		

SOURCE	barrel medic.
ORGANISM	Medicago truncatula
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
REFERENCE	1 (bases 1 to 804)
TITLE	Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores ,H.R., Imman,J.T., Weller,J.W., May,G.D. and Harrison,M.J. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula phosphate-starved leaf library Unpublished (2000) Contact: Harrison MJ Plant Biology Division The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7325 Fax: 580 221 7380 Email: mjharrison@noble.org Insert length: 804 Std Error: 0.00 Plate: 058 Row: H Column: 09 Seq primer: TCACACAGGAACGCTATGAC. Location/Qualifiers 1..804
JOURNAL	/organism="Medicago truncatula" /db_xref="taxon:3880" /clone="NF05BH09PL" /clone_lib="phosphate starved leaf" /lssue_type="leaf" /dev_stage="trifoliolate" /note="Vector: Lambda Zap; At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 hoaglands solution containing only 20um potassium phosphate. RNA was prepared from above ground tissues."
COMMENT	
FEATURES	
SOURCE	
BASE COUNT	215 a 202 c 181 g 165 t 41 others
ORIGIN	
Query Match	47.5%; Score 70.8; DB 14; Length 804;
Best Local Similarity	89.3%; Pred. No. 2,2e-13;
Matches	75; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY	49 AGTGGATCCCCCGGGCTCAGAGATTGCATTAAGCTTATGATACCGTCGACTCGAG 108 Db 81 AGTGATATCCCCCGGGCTCAGAGAAATTCATAACAGCTTATGATACCGTCNACCCTCGAG 140
OY	109 GGGGGGCTTAACTAACTAATTTTG 132
Db	141 GGGGGGCCCTGTGTTACCAATTTCTG 164
RESULT 6	
CNS07GJ4/c	
LOCUS	CNS07GJ4 128 bp DNA linear GSS 02-OCT-2001
DEFINITION	Anopheles gambiae GSS T7 end of clone 20K20 of library NotreDaniel from strain PEST of Anopheles gambiae (African malaria mosquito), genomic survey sequence.
ACCESSION	AL609826
VERSION	AL609826.1 GI:15916011
KEYWORDS	GSS.
SOURCE	African malaria mosquito.
ORGANISM	Anopheles gambiae Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles. 1 (bases 1 to 128) Genoscope. Direct Submission Submitted (01-OCT-2001) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - web : www.genoscope.cns.fr)
REFERENCE	2 (bases 1 to 128)
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
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RESULT 6	
CNS07GJ4/c	
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RESULT 6	
CNS07GJ4/c	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
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REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
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BASE COUNT	
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Query Match	
Best Local Similarity	
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RESULT 6	
CNS07GJ4/c	
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AUTHORS	
TITLE	
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Query Match	
Best Local Similarity	
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RESULT 6	
CNS07GJ4/c	
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DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
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ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
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FEATURES	
SOURCE	
BASE COUNT	
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Query Match	
Best Local Similarity	
Matches	
OY	
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CNS07GJ4/c	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
FEATURES	
SOURCE	
BASE COUNT	
ORIGIN	

LOCUS BE428068 162 bp mRNA linear EST 26-JUL-2000
 DEFINITION MTD002.H10F990615 ITEC MTD Durum wheat Root Library Triticum
 turgidum subsp. durum CDNA clone MTD002.H10, mRNA sequence.
 ACCESSION BE428068
 VERSION BE428068.1 GI:9425911
 KEYWORDS
 SOURCE EST.
 ORGANISM Triticum turgidum subsp. durum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 ; Triticeae; Triticum.
 1 (bases 1 to 162)
 Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier
 S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P.,
 Hermann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P.,
 Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y.,
 Peckhol,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M.,
 Sorrells,M., Warburton,M. and Wenzel,G.
 International Triticeae EST Cooperative (ITEC): Production of
 International Triticeae EST Cooperative (ITEC): Production of
 Expressed Sequence Tags for Species of the Triticeae
 Unpublished (2000)
 CONTACT: Joudrier P
 INRA, Unite de Biochimie et Biologie Molculaire des Cereales
 2, Place VIALA, 34060 Montpellier cedex 01 FRANCE
 Tel: 33 4 99 61 23 84
 Fax: 33 4 99 61 23 48
 Email: joudrier@enscm.inra.fr
 International Triticeae EST Cooperative (ITEC)
 http://wheat.pw.usda.gov/genome.
 Location/Qualifiers
 1..162
 /organism="Triticum turgidum subsp. durum"
 /cultivar="Silliana"
 /db_xref="taxon:4567"
 /clone_1id="MTD002.H10"
 /clone_1id="ITEC MTD Durum Wheat Root Library"
 /tissue_type="root"
 /dev_stage="3-day-old seedling, water-stressed"
 /note="vector: pSPORT1, T7 primers used. See pSPORT1
 polylinker site. 0.3-2.0 kbp average insert size."
 BASE COUNT 28 a 42 c 49 g 43 t
 ORIGIN

Query Match 47.0%; Score 70; DB 10; Length 162;
 Best Local Similarity 88.4%; Pred. No. 3.6e-13;
 Matches 76; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 49 AGTGATCCCCGGGCTGCAGAAATTCAGATTATCGATACCGTCGACCTCGAG 108
 |||||||
 DB 23 AGTGATCCCCGGGCTGCAGAAATTCAGATTATCGATACCGTCGACCTCGAG 82
 |||||||
 QY 109 GGGGGGCTTAACCTAATTTGTT 134
 |||||||
 DB 83 GGGGGGCTTAACCTAATTTGTT 108
 |||||||

RESULT 10
 AUC34451 390 bp mRNA linear EST 21-SEP-2001
 LOCUS AUC34451 Bovine placenta CDNA Bos taurus cDNA Cln1153 3',
 DEFINITION mRNA sequence.
 ACCESSION AUC34451
 VERSION AUC34451.1 GI:15719669
 KEYWORDS
 SOURCE EST.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 1 (bases 1 to 390)
 Gojima,H., Lejukole,H.Y., Taniguchi,Y., Yamada,T., Akagi,S., Yasue
 H. and Sasaki,Y.
 Analysis of expressed sequence tags from a cDNA library of bovine

JOURNAL placenta
 COMMENT Unpublished (2001)
 Contact: Takahisa Yamada
 Graduate School of Agriculture
 Kyoto University
 Sakyo-ku, Kitashirakawa, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-6323
 Fax: 81-75-753-6340
 Email: tyamada@kans.kyoto-u.ac.jp
 This clone was obtained from a 3' end cDNA library.
 Location/Qualifiers
 1..390
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_1id="Cln1153"
 /clone_1id="Bovine placenta CDNA"
 /tissue_type="placenta"
 /note="vector: pUC18 Sma I/BAP"
 BASE COUNT 113 a 77 c 72 g 128 t
 ORIGIN

Query Match 47.0%; Score 70; DB 9; Length 390;
 Best Local Similarity 88.4%; Pred. No. 3.9e-13;
 Matches 76; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 49 AGTGATCCCCGGGCTGCAGAAATTCAGATTATCGATACCGTCGACCTCGAG 108
 |||||||
 DB 299 AGTGATCCCCGGGCTGCAGAAATTCAGATTATCGATACCGTCGACCTCGAG 358
 |||||||
 QY 109 GGGGGGCTTAACCTAATTTGTT 134
 |||||||
 DB 359 GGGGGGCTTAACCTAATTTGTT 384
 |||||||

RESULT 11
 AUC278852 400 bp mRNA linear EST 02-JUL-2002
 LOCUS AUC278852 Cloned bovine placenta CDNA Bos taurus cDNA clone
 DEFINITION placenta1153 3', mRNA sequence.
 ACCESSION AUC278852
 VERSION AUC278852.1 GI:21682162
 KEYWORDS
 SOURCE EST.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 1 (bases 1 to 400)
 Oishi,M., Yamada,T., Goma,H., Lejukole,H.Y., Taniguchi,Y. and
 Sasaki,Y.
 EST analysis of cloned bovine fetus and placenta
 Unpublished (2002)
 Contact: Masahito Oishi
 Graduate School of Agriculture
 Kyoto University
 Sakyo-ku Kitashirakawa, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-6331
 Fax: 81-75-753-6340
 Email: oishi@kans.kyoto-u.ac.jp.
 Location/Qualifiers
 1..400
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_1id="placenta1153"
 /clone_1id="Cloned bovine placenta CDNA"
 /dev_stage="60 embryonic day"
 /note="Organ: ovary; Vector: pGEM-T Easy; Randomly cloned
 third differential products (DP3) of a Representational
 Differential Analysis (RDA) with bovine corpus luteum as
 tester tissue and skeletal muscle as driver."
 BASE COUNT 133 a 73 c 79 g 115 t
 ORIGIN

Query Match 47.0%; Score 70; DB 9; Length 400;
 Best Local Similarity 88.4%; Pred. No. 3.9e-13;
 Matches 76; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 49 AGTGATCCCCCGGCTGCAGAAATGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
 |||||
 DB 92 AGTGATCCCCCGGCTGCAGAAATGATATCAAGCTTATCGATACCGTCGACCTCGAG 33
 |||||

QY 109 GGGGGGCTTAACCTAATTTTGT 134
 |||||
 DB 32 GGGGGGCTTAACCTAATTTTGT 7
 |||||

RESULT 12
 LOCUS AO937400/c 864 bp DNA linear GSS 23-AUG-2000
 DEFINITION N82-011 Human NotI clones Homo sapiens genomic, DNA sequence.
 ACCESSION AO937400
 VERSION AO937400.1 GI:7213778
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 864)
 Zabarovsky,E.R., Gizatullin,R., Podowski,R.M., Zabarovska,V.V., Xie
 /, Muravenko,O.V., Kozlyrev,S., Petrenko,L., Skobeleva,N., Li,J.,
 Protopopov,A., Kashuba,V., Ernberg,I., Winberg,G. and Wahlestedt,C.
 NotI clones in the analysis of the human genome
 Nucleic Acids Res. 28 (7), 1635-1639 (2000)
 20175728
 Contact: Podowski RM
 Center for Genomics Research
 Karolinska Institute
 17177 Stockholm, Sweden
 Tel: +46-8-728-6372
 Fax: +46-8-337983
 Email: Raf.Podowski@cgrr.ki.se
 Class: NotI site.
 Location/Qualifiers
 1. 864
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Human NotI clones"
 /note="Organ: Lung; DNA was isolated from A549 cells after
 sodium arsenite exposure for 4 weeks. This fragment was
 differentially methylated relative to untreated controls
 and was identified using methylation sensitive AP-PCR and
 sequenced."

BASE COUNT 205 a 209 c 203 g 215 t 32 others

ORIGIN

Query Match 47.0%; Score 70; DB 17; Length 864;
 Best Local Similarity 88.4%; Pred. No. 4.2e-13;
 Matches 76; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 49 AGTGATCCCCCGGCTGCAGAAATGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
 |||||
 DB 151 AGTGATCCCCCGGCTGCAGAAATGATATCAAGCTTATCGATACCGTCGACCTCGAG 92
 |||||

QY 109 GGGGGGCTTAACCTAATTTTGT 134
 |||||
 DB 91 GGGGGGCTTAACCTAATTTTGT 66
 |||||

RESULT 13
 LOCUS BI306167/c 175 bp mRNA linear EST 20-JUL-2001
 DEFINITION NL_3_J08 Drought stress (leaf) Oryza sativa cDNA clone NL_3_J08 3',
 mRNA sequence.
 ACCESSION BI306167
 VERSION BI306167.1 GI:14981489
 KEYWORDS EST.

SOURCE
 ORGANISM
 Oryza sativa.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 175)
 Reddy,A.R., Ramakrishna,M., Chandrasekhar,A., Nagabhushan,I.,
 Ravindrababu,P. and Bennezen,J.L.
 Novel EST enrichment with normalized cDNA libraries from drought
 stressed rice (Oryza sativa L.cv Nagina 22)
 Unpublished (2001)
 Contact: Reddy AR
 Department of Plant Sciences, School of Life Sciences
 University of Hyderabad
 P.O. Central University, Hyderabad-500 046, A.P, India
 Tel: 0091-40-3010265
 Fax: 0091-40-3010145
 Email: arjuls@uohyd.ernet.in
 Insert Length: 175 Std Error: 0.00
 Plate: 3 row: 7 column: 08
 Seq primer: GTAAACGACGCGCGATG.
 Location/Qualifiers
 1. 175
 /organism="Oryza sativa"
 /cultivar="Nagina 22 (indica sub sp)"
 /db_xref="taxon:4530"
 /clone_lib="NL_3_J08"
 /clone_lib="Drought stress (leaf)"
 /tissue_type="entire leaf tissue"
 /dev_stage="35 day-old seedlings"
 /note="Organ: Leaf; Vector: T773Pac; ESTs from normalized
 leaf cDNA library from drought stressed seedlings"

BASE COUNT 32 a 47 c 50 g 46 t

ORIGIN

Query Match 46.8%; Score 69.8; DB 13; Length 175;
 Best Local Similarity 91.4%; Pred. No. 4.2e-13;
 Matches 74; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 49 AGTGATCCCCCGGCTGCAGAAATGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
 |||||
 DB 101 AGTGATCCCCCGGCTGCAGAAATGATATCAAGCTTATCGATACCGTCGACCTCGAG 42
 |||||

QY 109 GGGGGGCTTAACCTAATTT 129
 |||||
 DB 41 GGGGGGCTTAACCTAATTT 21
 |||||

RESULT 14
 LOCUS BI306149/c 182 bp mRNA linear EST 20-JUL-2001
 DEFINITION NL_3_I07 Drought stress (leaf) Oryza sativa cDNA clone NL_3_I07 3',
 mRNA sequence.
 ACCESSION BI306149
 VERSION BI306149.1 GI:14981471
 KEYWORDS EST.
 SOURCE Oryza sativa.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 182)
 Reddy,A.R., Ramakrishna,M., Chandrasekhar,A., Nagabhushan,I.,
 Ravindrababu,P. and Bennezen,J.L.
 Novel EST enrichment with normalized cDNA libraries from drought
 stressed rice (Oryza sativa L.cv Nagina 22)
 Unpublished (2001)
 Contact: Reddy AR
 Department of Plant Sciences, School of Life Sciences
 University of Hyderabad
 P.O. Central University, Hyderabad-500 046, A.P, India
 Tel: 0091-40-3010265
 Fax: 0091-40-3010145

Email: arjuls@uohyd.ernet.in
Insert Length: 182 Std Error: 0.00
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Seq primer: GTAAACGACGCCAGTG.

FEATURES

source

1. 182
/organism="Oryza sativa"
/cultivar="Nagina 22 (indica sub sp)"
/db_xref="taxon:4530"
/clone="NL_3_107"
/clone_lib="Drought stress (leaf)"
/tissue_type="Entire leaf tissue"
/dev_stage="35 day-old seedlings"
/note="Organ: Leaf; Vector: T7T3Pac; ESTs from normalized
leaf cDNA library from drought stressed seedlings "
BASE COUNT 35 a 47 c 52 g 48 t
ORIGIN

Query Match

Best Local Similarity 91.4%; Score 69.8; DB 13; Length 182;
Matches 74; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 49 AGTGGATCCCCGGGCTGCAGAAATTCGATATCGATACCTATCGACCTCGAG 108
|||||
DB 108 AGTGGATCCCCGGGCTGCAGAAATTCGATATCGATACCTATCGACCTCGAG 49
|||||

QY 109 GGGGGGCTTACTACTAATT 129
|||||

DB 48 GGGGGGCTCCGGTACCCAAATT 28

RESULT 15

BI306159/c

LOCUS NL_3_122 Drought stress (leaf) Oryza sativa cDNA clone NL_3_122 3',
DEFINITION mRNA sequence.

ACCESSION

BI306159
BI306159.1 GI:14981481

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 182)

REFERENCE

Reddy,A.R., Ramakrishna,W., Chandrasekhar,A., Nagabhushan,I.,
Ravindrababu,P. and Bennetzen,J.L.
Novel EST enrichment with normalized cDNA libraries from drought
stressed rice (Oryza sativa L.cv Nagina 22)

TITLE

Unpublished (2001)

JOURNAL

Contact: Reddy AR
Department of Plant Sciences, School of Life Sciences
University of Hyderabad

P.O. Central University, Hyderabad-500 046, A.P, India

Tel: 0091-40-3010265

Fax: 0091-40-3010145

Email: arjuls@uohyd.ernet.in

Insert Length: 182 Std Error: 0.00

FEATURES

source

1. 182

Location/Qualifiers

/organism="Oryza sativa"

/cultivar="Nagina 22 (indica sub sp)"

/db_xref="taxon:4530"

/clone="NL_3_122"

/clone_lib="Drought stress (leaf)"

/tissue_type="Entire leaf tissue"

/dev_stage="35 day-old seedlings"

/note="Organ: Leaf; Vector: T7T3Pac; ESTs from normalized
leaf cDNA library from drought stressed seedlings "

BASE COUNT 36 a 47 c 52 g 46 t

ORIGIN

Query Match 46.8%; Score 69.8; DB 13; Length 182;
Best Local Similarity 91.4%; Pred. No. 4.3e-13;
Matches 74; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 49 AGTGGATCCCCGGGCTGCAGAAATTCGATATCGATACCTATCGACCTCGAG 108
|||||

DB 108 AGTGGATCCCCGGGCTGCAGAAATTCGATATCGATACCTATCGACCTCGAG 49
|||||

QY 109 GGGGGGCTTACTACTAATT 129
|||||

DB 48 GGGGGGCTCCGGTACCCAAATT 28

Search completed: November 10, 2002, 08:33:11
Job time : 1342 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 04:19:15 ; Search time 175.807 Seconds
(without alignments)
1908.619 Million cell updates/sec

Title: US-08-935-377-8
Sequence: 1 GGCCAAATGCAAAACTA.....TTGTTTGTGCGCCCGGCC 149

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	149	100.0	149	21	AAA15237
2	149	100.0	149	22	ABA01478
3	149	100.0	149	24	AAD31780
4	138	92.6	150	21	AAA15238
5	138	92.6	150	22	ABA01479
6	138	92.6	150	24	AAD31781
7	137	91.9	148	21	AAA15236
8	137	91.9	148	22	ABA01477
9	137	91.9	148	24	AAD31779

10	131	87.9	145	21	AAA15235	Nucleotide sequenc
11	131	87.9	145	22	ABA01476	Partial p7.5/ATG0/
12	131	87.9	145	24	AAD31778	Modified p7.5/tk v
13	75.6	50.7	508	23	ABV39281	Human prostate exp
14	74	49.7	380	23	ABV36219	Human prostate exp
15	74	49.7	380	23	ABV45265	Human prostate exp
16	73.4	49.3	437	23	ABV38437	Human prostate exp
17	73.2	49.1	462	23	ABV32112	Human prostate exp
18	73	49.0	611	23	ABV42990	Human prostate exp
19	73	49.0	612	23	ABV34128	Human prostate exp
20	72.8	48.9	684	23	ABV36344	Human prostate exp
21	72.8	48.9	684	23	ABV45375	Human prostate exp
22	72.6	48.7	460	23	ABV33323	Human prostate exp
23	72.6	48.7	460	23	ABV42246	Human prostate exp
24	72.4	48.6	372	23	ABV43508	Human prostate exp
25	72.4	48.6	467	23	ABV45888	Human prostate exp
26	72.4	48.6	528	23	ABV38666	Human prostate exp
27	72.2	48.5	638	23	ABV44137	Human prostate exp
28	71.8	48.2	475	23	ABV30533	Human prostate exp
29	71.8	48.2	475	23	ABV39505	Human prostate exp
30	71.6	48.1	333	23	ABV45519	Human prostate exp
31	71.6	48.1	392	23	ABV38605	Human prostate exp
32	71.6	48.1	455	23	ABV31882	Human prostate exp
33	71.6	48.1	459	23	ABV35787	Human prostate exp
34	71.6	48.1	459	23	ABV44587	Human prostate exp
35	71.6	48.1	552	23	ABV35639	Human prostate exp
36	71.6	48.1	659	23	ABV39144	Human prostate exp
37	71.6	48.1	659	23	ABV45482	Human prostate exp
38	71.6	48.1	659	23	ABV45486	Human prostate exp
39	71.4	47.9	276	23	ABV35118	Human prostate exp
40	71.4	47.9	375	23	ABV44301	Human prostate exp
41	71.4	47.9	408	23	ABV35367	Human prostate exp
42	71.4	47.9	410	23	ABV32098	Human prostate exp
43	71.4	47.9	410	23	ABV38443	Human prostate exp
44	71.4	47.9	410	23	ABV41036	Human prostate exp
45	71.4	47.9	436	23	ABV38427	Human prostate exp

ALIGNMENTS

RESULT 1
AAA15237
ID AAA15237 standard; DNA; 149 BP.
XX
XX AAA15237:
XX
XX 04-SEP-2000 (first entry)
XX
XX Nucleotide sequence of a fragment of the plasmid p7.5/ATG2/tk.
XX
XX Vaccinia transfer plasmid; epitope; tumour specific epitope; antigen;
XX
XX vaccine; tumour regression; cancer; infection; ss.
XX
XX Synthetic.
XX
XX WO200028016-A1.
XX
XX 18-MAY-2000.
XX
XX 10-NOV-1998; 98WO-US24029.
XX
XX 10-NOV-1998; 98WO-US24029.
XX
XX 10-NOV-1998; 98WO-US24029.
XX
XX (VYRP) UNIV ROCHESTER.
XX
XX Zauderer M;
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XX WPI: 2000-376533/32.
XX
XX Novel method of identifying target epitopes or antigens specific for
XX human tumors, cancers and infected cells involving screening expression
XX library products of a cell expressing the target epitope

```
XX PS Disclosure; Fig 2; 132pp; English.
XX CC
XX CC The present sequence represents a fragment of a vaccinia transfer
XX CC plasmid, which is used in the course of the invention. The
XX CC specification describes a method for identifying a target epitope.
XX CC The method comprises screening the products of an expression library
XX CC from a cell expressing the target epitope with cytotoxic T cells
XX CC generated against the cell to identify DNA clones expressing the target
XX CC epitope. The method may also comprise providing a cytotoxic T cell
XX CC specific for a gene product differentially expressed by a cell and
XX CC measuring the cross-reactivity of the cytotoxic T cell. The methods are
XX CC useful for identifying tumour specific target epitopes and antigens which
XX CC are useful in immunogenic compositions or vaccines to induce the
XX CC regression of tumours, cancers or infections in mammals. The genes
XX CC expressed in a panel of tumour cells that are derived from single
XX CC immortalised, non-tumorigenic cell line are used to generate HLA
XX CC restricted cytotoxic T cells which are evaluated for activity against
XX CC tumour cells. The method is useful to identify potential antigens
XX CC expressed not only by the pathogen but also by the host cells whose gene
XX CC expression is altered as a result of infection. The differential gene
XX CC expression strategies can be applied to identify immunogenic molecules
XX CC of cells infected with virus, fungus or mycobacterium.
XX SQ Sequence 149 BP; 36 A; 37 C; 39 G; 37 T; 0 other;
XX
XX Query Match 100.0%; Score 149; DB 21; Length 149;
XX Best Local Similarity 100.0%; Pred. No. 1,7e-41;
XX Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GGGCAAAAATTTGAAAATCTAGATCTATTATTGACGCGCGCCGCATGAGTGATCCCC 60
XX DB 1 GGGCAAAAATTTGAAAATCTAGATCTATTATTGACGCGCGCCGCATGAGTGATCCCC 60
XX
XX QY 61 GGGCTGCGAGAAATTCGATTCAGAGCTTATGACGCGCGCCGCATGAGTGATCCCC 120
XX DB 61 GGGCTGCGAGAAATTCGATTCAGAGCTTATGACGCGCGCCGCATGAGTGATCCCC 120
XX
XX QY 121 TAACATAATTTGTTTGTGTGGCGCGCC 149
XX DB 121 TAACATAATTTGTTTGTGTGGCGCGCC 149
XX
XX RESULT 2
XX ID ABA01478 standard; DNA; 149 BP.
XX AC ABA01478;
XX DT 04-FEB-2002 (first entry)
XX DE Partial p7.5/ATG2/Ck sequence.
XX OS
XX KW Cell death; toxic gene; tumour suppressor; ds.
XX OS Synthetic.
XX OS WO200172995-A2.
XX PD 04-OCT-2001.
XX PF 28-MAR-2001; 2001WO-US09953.
XX PR 28-MAR-2000; 2000US-0192586.
XX PR 10-MAY-2000; 2000US-0203343.
XX PR 23-JAN-2001; 2001US-0263226.
XX PR 27-FEB-2001; 2001US-0271426.
XX PA (UVRP ) UNIV ROCHESTER.
XX PI Zauderer M, Smith ES;
XX DR WPI; 2001.570897/64.
```

```
XX PT Selecting target polynucleotides, particularly toxic genes, involves
XX PT introducing a library of insert polynucleotides into a host cell
XX PT population, where the target polynucleotide promotes cell death -
XX PS Disclosure; Fig 8; 359pp; English.
XX CC
XX CC The present invention relates to a method for selecting a target
XX CC polynucleotide. The method comprises introducing into a host cell
XX CC population a library of insert polynucleotides, where expression of the
XX CC target polynucleotide directly or indirectly promotes host cell death.
XX CC The cells are cultured and the insert polynucleotides are collected from
XX CC the cells which die. The method is useful for selecting target
XX CC polynucleotides, particularly polynucleotides which alter cell phenotypes
XX CC of induce or inhibit cell death. The method can be used to isolate toxic
XX CC genes such as tumour suppressors. The present sequence was used to
XX CC illustrate the method of the the present invention.
XX SQ Sequence 149 BP; 36 A; 37 C; 39 G; 37 T; 0 other;
XX
XX Query Match 100.0%; Score 149; DB 22; Length 149;
XX Best Local Similarity 100.0%; Pred. No. 1,7e-41;
XX Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GGGCAAAAATTTGAAAATCTAGATCTATTATTGACGCGCGCCGCATGAGTGATCCCC 60
XX DB 1 GGGCAAAAATTTGAAAATCTAGATCTATTATTGACGCGCGCCGCATGAGTGATCCCC 60
XX
XX QY 61 GGGCTGCGAGAAATTCGATTCAGAGCTTATGACGCGCGCCGCATGAGTGATCCCC 120
XX DB 61 GGGCTGCGAGAAATTCGATTCAGAGCTTATGACGCGCGCCGCATGAGTGATCCCC 120
XX
XX QY 121 TAACATAATTTGTTTGTGTGGCGCGCC 149
XX DB 121 TAACATAATTTGTTTGTGTGGCGCGCC 149
XX
XX RESULT 3
XX ID AAD31780 standard; DNA; 149 BP.
XX AC AAD31780;
XX DT 18-JUN-2002 (first entry)
XX DE Modified p7.5/Ck vector, p7.5/ATG2/Ck.
XX OS
XX KW Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;
XX KW vaccine; immune response; cytostatic; p7.5/Ck vector; thymidine kinase;
XX KW p7.5/ATG2/Ck vector; ds.
XX OS Synthetic.
XX OS Vaccinia virus.
XX OS
XX FH Key Location/Qualifiers
XX FT misc_signal 46..48
XX FT /tag= a
XX FT /note= "translation start codon"
XX FT 117..119
XX FT /tag= b
XX FT /note= "translation stop codon"
XX FT 121..123
XX FT /tag= c
XX FT /note= "translation stop codon"
XX FT 125..127
XX FT /tag= d
XX FT /note= "translation stop codon"
XX FT 133..139
XX FT /tag= e
XX FT /note= "transcription stop signal"
XX PN US2002018765-A1.
```

PD 14-FEB-2002.
XX
PF 02-APR-2001; 2001US-0822250.
XX
PR 22-SEP-1997; 97US-0935377.
XX
PA (UYRP) UNIV ROCHESTER.
XX
PI Zauderer M;
XX
DR WPI; 2002-239252/29.
XX
PT Representational Difference Analysis method for identification of
PT antigens recognized by cytotoxic T cells and specific for human tumors,
PT comprises improved selection of genes encoding target antigens -
XX
PS Example 1; Fig 2; 54pp; English.
XX
CC The present invention relates to novel methods for the identification
CC of antigens recognised by cytotoxic T cells (CTLs) and specific for
CC human tumours, cancers and infected cells. The method involves screening
CC the products of an expression library generated from DNA/RNA of a cell
CC expressing a target epitope with cytotoxic T cells generated against
CC the cell to identify DNA clones expressing target epitope or providing
CC cytotoxic T cells specific for a gene product differentially expressed
CC by a cell and measuring the cross-reactivity of the cytotoxic T cells
CC for cells expressing a target epitope in which the target epitope is
CC identified as a gene product inducing cytotoxic T cells. The method is
CC useful for identifying a target epitope or antigen specific for a tumour
CC cell. The target epitope is also useful for identifying target antigens
CC in other target cells against which it is desirable to induce cell-
CC mediated immunity. The antigen identified by the method is useful
CC in immunogenic compositions and vaccine preparations to induce the
CC regression of tumours, cancers and infections in mammals. The invention
CC also relates to vaccinia viral vectors which are useful for treating
CC tumour-bearing mammals, including humans to generate immune response
CC against the tumour cells. They are also useful for immunising or
CC vaccinating tumour-free subjects to prevent tumour formation. The
CC present sequence is modified p7.5/tk (thymidine kinase) vector,
CC p7.5/ATG2/tk. This vector comprises a vaccinia virus 7.5K promoter and
CC a modified tk DNA fragment. This vector is used in the exemplification
CC of the invention.
XX
SQ Sequence 149 BP; 36 A; 37 C; 39 G; 37 T; 0 other;
XX
Query Match 100.0%; Score 149; DB 24; Length 149;
Best Local Similarity 100.0%; Pred. No. 1.7e-41;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGCCAAAATGAAAACCTAGATCTATTATTGACGCGCGCCGCGCATGAGTGCATCCCC 60
DB 1 GGCCAAAATGAAAACCTAGATCTATTATTGACGCGCGCGCCGCGCATGAGTGCATCCCC 60
QY 61 GGGCTGCAGAAATTCGATATCAAGCTTATCGATCGTCGACCTCGAGGGGGGCGCTAAC 120
DB 61 GGGCTGCAGAAATTCGATATCAAGCTTATCGATCGTCGACCTCGAGGGGGGCGCTAAC 120
QY 121 TAACTAATTTTGTGTTTGTGGGCGCGCC 149
DB 121 TAACTAATTTTGTGTTTGTGGGCGCGCC 149
XX
RESULT 4
AAAI5238
ID AAI5238 standard; DNA; 150 BP.
XX
AC AAI5238;
XX
DT 04-SEP-2000 (first entry)
XX
DE Nucleotide sequence of a fragment of the plasmid p7.5/ATG3/tk.
XX
KM Vaccinia transfer plasmid; epitope; tumour specific epitope; antigen;

KM vaccine; tumour regression; cancer; infection; ss.
XX
XX Synthetic.
OS
XX
PN WO200028016-A1.
XX
XX 18-MAY-2000.
PD
XX
XX 10-NOV-1998; 98WO-US24029.
XX
PF 10-NOV-1998; 98WO-US24029.
PR 10-NOV-1998; 98WO-US24029.
XX
PA (UYRP) UNIV ROCHESTER.
XX
PI Zauderer M;
XX
DR WPI; 2000-376533/32.
XX
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PT human tumors, cancers and infected cells involving screening expression
PT library products of a cell expressing the target epitope -
XX
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CC plasmid, which is used in the course of the invention. The
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CC from a cell expressing the target epitope with cytotoxic T cells
CC generated against the cell to identify DNA clones expressing the target
CC epitope. The method may also comprise providing a cytotoxic T cell
CC specific for a gene product differentially expressed by a cell and
CC measuring the cross-reactivity of the cytotoxic T cell. The methods are
CC useful for identifying tumour specific target epitopes and antigens which
CC are useful in immunogenic compositions or vaccines to induce the
CC regression of tumors, cancers or infections in mammals. The genes
CC expressed in a panel of tumour cells that are derived from single
CC immortalised, non-tumorigenic cell line are used to generate HLA
CC restricted cytotoxic T cells which are evaluated for activity against
CC tumour cells. The method is useful to identify potential antigens
CC expressed not only by the pathogen but also by the host cells whose gene
CC expression is altered as a result of infection. The differential gene
CC expression strategies can be applied to identify immunogenic molecules
CC of cells infected with virus, fungus or mycobacterium.
XX
SQ Sequence 150 BP; 36 A; 38 C; 39 G; 37 T; 0 other;
XX
Query Match 92.6%; Score 138; DB 21; Length 150;
Best Local Similarity 99.3%; Pred. No. 1.1e-37;
Matches 149; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 GGCCAAAATGAAAACCTAGATCTATTATTGACGCGCGCCGCGCATGAGTGCATCCCC 59
DB 1 GGCCAAAATGAAAACCTAGATCTATTATTGACGCGCGCGCCGCGCATGAGTGCATCCCC 60
QY 60 GGGCTGCAGAAATTCGATATCAAGCTTATCGATCGTCGACCTCGAGGGGGGCGCTAAC 119
DB 61 GGGCTGCAGAAATTCGATATCAAGCTTATCGATCGTCGACCTCGAGGGGGGCGCTAAC 120
QY 120 CTACTAATTTTGTGTTTGTGGGCGCGCC 149
DB 121 CTACTAATTTTGTGTTTGTGGGCGCGCC 150
XX
RESULT 5
ABA01479
ID ABA01479 standard; DNA; 150 BP.
XX
AC ABA01479;
XX
DT 04-FEB-2002 (first entry)
XX
DE Partial p7.5/ATG3/tk sequence.

```
XX Cell death; toxic gene; tumour suppressor; ds.
KM Synthetic.
OS WO200172995-A2.
XX 04-OCT-2001.
XX 28-MAR-2001: 2001WO-US09953.
XX 28-MAR-2000: 2000US-0192586.
XX 10-MAY-2000: 2000US-0203343.
XX 23-JAN-2001: 2001US-0263226.
XX 27-FEB-2001: 2001US-0271426.
XX (UYRP ) UNIV ROCHESTER.
XX Zauderer M, Smith ES;
XX WPI; 2001-570897/64.
XX
XX Selecting target polynucleotides, particularly toxic genes, involves
XX introducing a library of insert polynucleotides into a host cell
XX population, where the target polynucleotide promotes cell death -
XX Disclosure; Fig 8; 359pp; English.
XX
XX The present invention relates to a method for selecting a target
XX polynucleotide. The method comprises introducing into a host cell
XX a population a library of insert polynucleotides, where expression of the
XX target polynucleotide directly or indirectly promotes host cell death.
XX The cells are cultured and the insert polynucleotides are collected from
XX the cells which die. The method is useful for selecting target
XX polynucleotides, particularly polynucleotides which alter cell phenotypes
XX of induce or inhibit cell death. The method can be used to isolate toxic
XX genes such as tumour suppressors. The present sequence was used to
XX illustrate the method of the the present invention.
XX
XX Sequence 150 BP; 36 A; 38 C; 39 G; 37 T; 0 other;
XX
XX Query Match 92.6%; Score 138; DB 22; Length 150;
XX Best Local Similarity 99.3%; Pred. No. 1.1e-37;
XX Matches 149; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
XX 1 GGCCAAAATGAAAACAGATCTATTATTCGACGCGCGCCCATGA-GTGGATCCCC 59
XX |||||||||||||||||||||||||||||||||||||||||||||||||||
XX 1 GGCCAAAATGAAAACAGATCTATTATTCGACGCGCGCCCATGA-GTGGATCCCC 60
XX
XX 60 CGGCGTCGAGAAATTCGATATCAAGCTTATCGATACCGTCGAGGGGGGCTTAA 119
XX |||||||||||||||||||||||||||||||||||||||||||||||||||
XX 61 CGGCGTCGAGAAATTCGATATCAAGCTTATCGATACCGTCGAGGGGGGCTTAA 120
XX
XX 120 CTAACTAATTTTGTGTTTGGCGCCGCC 149
XX |||||||||||||||||||||||||||
XX 121 CTAACTAATTTTGTGTTTGGCGCCGCC 150
XX
XX RESULT 6
XX AAD31781
XX ID AAD31781 standard; DNA: 150 BP.
XX
XX AAD31781:
XX
XX 18-JUN-2002 (first entry)
XX
XX Modified p7.5/tk vector, p7.5/ATG3/tk.
XX
XX Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;
XX vaccine; immune response; cytostatic; p7.5/tk vector; thymidine kinase;
XX p7.5/ATG3/tk vector; ds.
XX
XX Vaccinia virus.
XX
OS
```

```
OS Synthetic.
XX Location/Qualifiers
XX Key 46..48
XX misc_signal /*tag= a
XX /*note= "Translation start codon"
XX 118..120
XX misc_signal /*tag= b
XX /*note= "Translation stop codon"
XX 122..124
XX misc_signal /*tag= c
XX /*note= "Translation stop codon"
XX 126..128
XX misc_signal /*tag= d
XX /*note= "Translation stop codon"
XX 134..140
XX misc_signal /*tag= e
XX /*note= "Transcription stop signal"
XX
XX US2002018785-A1.
XX
XX 14-FEB-2002.
XX
XX 02-APR-2001: 2001US-0822250.
XX
XX 22-SEP-1997: 97US-0935377.
XX
XX (UYRP ) UNIV ROCHESTER.
XX
XX Zauderer M;
XX WPI; 2002-239252/29.
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XX Representational Difference Analysis method for identification of
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XX comprises improved selection of genes encoding target antigens -
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XX of antigens recognised by cytotoxic T cells (CTLs) and specific for
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XX the products of an expression library generated from DNA/RNA of a cell
XX expressing a target epitope with cytotoxic T cells generated against
XX the cell to identify DNA clones expressing target epitope or providing
XX cytotoxic T cells specific for a gene product differentially expressed
XX by a cell and measuring the cross-reactivity of the cytotoxic T cells
XX for cells expressing a target epitope in which the target epitope is
XX identified as a gene product inducing cytotoxic T cells. The method is
XX useful for identifying a target epitope or antigen specific for a tumour
XX cell. The target epitope is also useful for identifying target antigens
XX in other target cells against which it is desirable to induce cell-
XX mediated immunity. The antigen identified by the method is useful
XX in immunogenic compositions and vaccine preparations to induce the
XX regression of tumours, cancers and infections in mammals. The invention
XX also relates to vaccinia viral vectors which are useful for treating
XX tumour-bearing mammals, including humans to generate immune response
XX against the tumour cells. They are also useful for immunising or
XX vaccinating tumour-free subjects to prevent tumour formation. The
XX present sequence is modified p7.5/tk (thymidine kinase) vector,
XX p7.5/ATG3/tk. This vector comprises a vaccinia virus 7.5k promoter and
XX a modified tk DNA fragment. This vector is used in the exemplification
XX of the invention.
XX
XX Sequence 150 BP; 36 A; 38 C; 39 G; 37 T; 0 other;
XX
XX Query Match 92.6%; Score 138; DB 24; Length 150;
XX Best Local Similarity 99.3%; Pred. No. 1.1e-37;
XX Matches 149; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
XX 1 GGCCAAAATGAAAACAGATCTATTATTCGACGCGCGCCCATGA-GTGGATCCCC 59
XX |||||||||||||||||||||||||||||||||||||||||||||||||||
XX 1 GGCCAAAATGAAAACAGATCTATTATTCGACGCGCGCCCATGA-GTGGATCCCC 60
XX
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```
OY 60 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCTTAA 119
    |||||||
DB 61 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCTTAA 120
OY 120 CTAATTAATTTGTTTGTGTGGCCCGGCC 149
    |||||||
DB 121 CTAATTAATTTGTTTGTGTGGCCCGGCC 150

RESULT 7
AAAI5236
ID AAI5236 standard; DNA; 148 BP.
AC AAI5236;
XX
DT 04-SEP-2000 (first entry)
DE Nucleotide sequence of a fragment of the plasmid p7.5/MTG1/tk.
XX
KW Vaccinia transfer plasmid; epitope; tumour specific epitope; antigen;
KM vaccine; tumour regression; cancer; infection; ss.
XX
OS Synthetic.
XX
PN WO200028016-A1.
PD 18-MAY-2000.
XX
PF 10-NOV-1998; 98WO-US24029.
XX
PR 10-NOV-1998; 98WO-US24029.
XX
PA (UVRP ) UNIV ROCHESTER.
PI Zauderer M;
XX
DR WPI; 2000-376533/32.
XX
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PT human tumors, cancers and infected cells involving screening expression
PT library products of a cell expressing the target epitope -
XX
XX Disclosure; Fig 2; 132pp; English.
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CC specific for a gene product differentially expressed by a cell and
CC measuring the cross-reactivity of the cytotoxic T cell. The methods are
CC useful for identifying tumour specific target epitopes and antigens which
CC are useful in immunogenic compositions or vaccines to induce the
CC regression of tumors, cancers or infections in mammals. The genes
CC expressed in a panel of tumour cells that are derived from single
CC immunotised, non-tumorigenic cell line are used to generate HLA
CC restricted cytotoxic T cells which are evaluated for activity against
CC tumour cells. The method is useful to identify potential antigens
CC expressed not only by the pathogen but also by the host cells whose gene
CC expression is altered as a result of infection. The differential gene
CC expression strategies can be applied to identify immunogenic molecules
CC of cells infected with virus, fungus or mycobacterium.
XX
SQ Sequence 148 BP; 35 A; 37 C; 39 G; 37 T; 0 other;

Query Match 91.9%; Score 137; DB 21; Length 148;
Best Local Similarity 99.3%; Pred. No. 2.3e-37;
Matches 148; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

```
OY 60 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCTTAA 119
    |||||||
DB 61 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCTTAA 120
OY 120 CTAATTAATTTGTTTGTGTGGCCCGGCC 149
    |||||||
DB 120 TAACTAATTTGTTTGTGTGGCCCGGCC 148

RESULT 8
ABA01477
ID ABA01477 standard; DNA; 148 BP.
AC ABA01477;
XX
DT 04-FEB-2002 (first entry)
DE Partial p7.5/MTG1/tk sequence.
XX
KW Cell death; toxic gene; tumour suppressor; ds.
XX
OS Synthetic.
XX
PN WO200172995-A2.
PD 04-OCT-2001.
XX
PF 28-MAR-2001; 2001WO-US09953.
XX
PR 28-MAR-2000; 2000US-0192586.
PR 10-MAY-2000; 2000US-0203343.
PR 23-JAN-2001; 2001US-0263226.
PR 27-FEB-2001; 2001US-0271426.
XX
PA (UVRP ) UNIV ROCHESTER.
PI Zauderer M, Smith ES;
XX
DR WPI; 2001-570897/64.
XX
PT Selecting target polynucleotides, particularly toxic genes, involves
PT introducing a library of insert polynucleotides into a host cell
PT population, where the target polynucleotide promotes cell death -
XX
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CC polynucleotide. The method comprises introducing into a host cell
CC population a library of insert polynucleotides, where expression of the
CC target polynucleotide directly or indirectly promotes host cell death.
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CC the cells which die. The method is useful for selecting target
CC polynucleotides, particularly polynucleotides which alter cell phenotypes
CC of induce or inhibit cell death. The method can be used to isolate toxic
CC genes such as tumour suppressors. The present sequence was used to
CC illustrate the method of the the present invention.
XX
SQ Sequence 148 BP; 35 A; 37 C; 39 G; 37 T; 0 other;

Query Match 91.9%; Score 137; DB 22; Length 148;
Best Local Similarity 99.3%; Pred. No. 2.3e-37;
Matches 148; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```


CC specific for a gene product differentially expressed by a cell and
 CC measuring the cross-reactivity of the cytotoxic T cell. The methods are
 CC useful for identifying tumor specific target epitopes and antigens which
 CC are useful in immunogenic compositions or vaccines to induce the
 CC regression of tumors, cancers or infections in mammals. The genes
 CC expressed in a panel of tumor cells that are derived from single
 CC immortalised, non-tumourigenic cell line are used to generate HLA
 CC restricted cytotoxic T cells which are evaluated for activity against
 CC tumor cells. The method is useful to identify potential antigens
 CC expressed not only by the pathogen but also by the host cells whose gene
 CC expression is altered as a result of infection. The differential gene
 CC expression strategies can be applied to identify immunogenic molecules
 CC of cells infected with virus, fungus or mycobacterium.

SO Sequence 145 BP; 34 A; 37 C; 38 G; 36 T; 0 other;

Query Match 87.9%; Score 131; DB 21; Length 145;
 Best Local Similarity 97.3%; Pred. No. 2.7e-35;

Matches 145; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

OY 1 GGGCAAAATTTGAAACTAGATCTATTATTGACGCGCGCCCATGAGTGATCCCCC 60
 DB 1 GGGCAAAATTTGAAACTAGATCTATTATTGACGCGCGCCCATGAGTGATCCCCC 56
 OY 61 GGGCTGCAGGAATTCGATATCAAGCTTATGATACCGTCGACCTCGAGGGGGGCGCTTAC 120
 DB 57 GGGCTGCAGGAATTCGATATCAAGCTTATGATACCGTCGACCTCGAGGGGGGCGCTTAC 116
 OY 121 TAACATAATTTGTTTTGTGGCGCCGCC 149
 DB 117 TAACATAATTTGTTTTGTGGCGCCGCC 145

RESULT 11

ABA01476
 ID ABA01476 standard; DNA; 145 BP.

AC ABA01476;

DT 04-FEB-2002 (first entry)

DE Partial p7.5/ATG0/tk sequence.

KW Cell death; toxic gene; tumour suppressor; ds.

OS Synthetic.

PN W0200172995-A2.

PD 04-OCT-2001.

PF 28-MAR-2001; 2001MO-US09953.

PR 28-MAR-2000; 2000US-0192586.

PR 10-MAY-2000; 2000US-0203343.

PR 23-JAN-2001; 2001US-0263226.

PR 27-FEB-2001; 2001US-0271426.

PA (UTRP) UNIV ROCHESTER.

PI Zauderer M, Smith ES;

DR WPI; 2001-570897/64.

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 PT population, where the target polynucleotide promotes cell death -
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 CC the cells which die. The method is useful for selecting target
 CC polynucleotides, particularly polynucleotides which alter cell phenotypes
 CC of induce or inhibit cell death. The method can be used to isolate toxic
 CC genes such as tumour suppressors. The present sequence was used to
 CC illustrate the method of the the present invention.

SO Sequence 145 BP; 34 A; 37 C; 38 G; 36 T; 0 other;

Query Match 87.9%; Score 131; DB 22; Length 145;
 Best Local Similarity 97.3%; Pred. No. 2.7e-35;
 Matches 145; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

OY 1 GGGCAAAATTTGAAACTAGATCTATTATTGACGCGCGCCCATGAGTGATCCCCC 60
 DB 1 GGGCAAAATTTGAAACTAGATCTATTATTGACGCGCGCCCATGAGTGATCCCCC 56
 OY 61 GGGCTGCAGGAATTCGATATCAAGCTTATGATACCGTCGACCTCGAGGGGGGCGCTTAC 120
 DB 57 GGGCTGCAGGAATTCGATATCAAGCTTATGATACCGTCGACCTCGAGGGGGGCGCTTAC 116
 OY 121 TAACATAATTTGTTTTGTGGCGCCGCC 149
 DB 117 TAACATAATTTGTTTTGTGGCGCCGCC 145

RESULT 12

AAD31778
 ID AAD31778 standard; DNA; 145 BP.

AC AAD31778;

DT 18-JUN-2002 (first entry)

DE Modified p7.5/tk vector, p7.5/ATG0/tk.

KW Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;
 KW vaccine; immune response; cytostatic; p7.5/tk vector; thymidine kinase;
 KW p7.5/ATG0/tk vector; ds.

OS Vaccinia virus.

OS Synthetic.

FH Key Location/Qualifiers

FT misc_signal 113..115

FT /*tag= a

FT /*note= "translation stop codon"

FT misc_signal 117..119

FT /*tag= b

FT /*note= "translation stop codon"

FT misc_signal 121..123

FT /*tag= c

FT /*note= "translation stop codon"

FT misc_signal 129..135

FT /*tag= d

FT /*note= "transcription stop signal"

US2002018785-A1.

14-FEB-2002.

02-APR-2001; 2001US-0822250.

22-SEP-1997; 97US-0935377.

(UTRP) UNIV ROCHESTER.

Zauderer M;

WPI; 2002-239252/29.

Representational Difference Analysis method for identification of

PT antitumors recognized by cytotoxic T cells and specific for human tumors,
CC comprises improved selection of genes encoding target antigens -
XX
PS Example 1; Fig 2; 54pp; English.
CC The present invention relates to novel methods for the identification
CC of antigens recognised by cytotoxic T cells (CTLs) and specific for
CC human tumours, cancers and infected cells. The method involves screening
CC the products of an expression library generated from DNA/RNA of a cell
CC expressing a target epitope with cytotoxic T cells generated against
CC the cell to identify DNA clones expressing target epitope or providing
CC cytotoxic T cells specific for a gene product differentially expressed
CC by a cell and measuring the cross-reactivity of the cytotoxic T cells
CC for cells expressing a target epitope in which the target epitope is
CC identified as a gene product inducing cytotoxic T cells. The method is
CC useful for identifying a target epitope or antigen specific for a tumour
CC cell. The target epitope is also useful for identifying target antigens
CC in other target cells against which it is desirable to induce cell-
CC mediated immunity. The antigen identified by the method is useful
CC in immunogenic compositions and vaccine preparations to induce the
CC regression of tumours, cancers and infections in mammals. The invention
CC also relates to vaccinia viral vectors which are useful for treating
CC tumour-bearing mammals, including humans to generate immune response
CC against the tumour cells. They are also useful for immunising or
CC vaccinating tumour-free subjects to prevent tumour formation. The
CC present sequence is modified p7.5/tk (thymidine kinase) vector.
CC p7.5/ARGO/tk. This vector comprises a vaccinia virus 7.5k promoter and
CC a modified tk DNA fragment. This vector is used in the exemplification
CC of the invention.
XX
SQ Sequence 145 BP; 34 A; 37 C; 38 G; 36 T; 0 other;
XX
Query Match 87.9%; Score 131; DB 24; Length 145;
Best Local Similarity 97.3%; Pred. No. 2.7e-35;
Matches 145; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
XX
QY 1 GGGCAAAATGAAACTAGATCTATTATTGACGCGCGCCGATGATGATGCC 60
DB 1 GGGCAAAATGAAACTAGATCTATTATTGACGCGCGCCGATGATGATGCC 56
XX
QY 61 GGGCTGCAGGATTCGATATCAAGCTTATCGATACCGTGCAGCTCGAGGGGGGCTTAAC 120
DB 57 GGGCTGCAGGATTCGATATCAAGCTTATCGATACCGTGCAGCTCGAGGGGGGCTTAAC 116
XX
QY 121 TAACTAATTTGTTTGTGGGCGCGGCC 149
DB 117 TAACTAATTTGTTTGTGGGCGCGGCC 145
XX
RESULT 13
ABV39281
ID ABV39281 standard; cDNA; 508 BP.
XX
AC ABV39281;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 39272.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 18-JUL-2000; 2000US-219007P.

PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PS (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI, 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 7972; 11750pp; English.
XX
SQ The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 508 BP; 140 A; 115 C; 125 G; 128 T; 0 other;
XX
Query Match 50.7%; Score 75.6; DB 23; Length 508;
Best Local Similarity 85.7%; Pred. No. 4.7e-16;
Matches 84; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
XX
QY 37 GCGGCGCCATGAGTATGATCCCGGGGCTGCGAGATTCGATATCAAGCTTATGATACC 96
DB 207 GCGGCGCTCGAGATGATGATCCCGGGGCTGCGAGATTCGATATCAAGCTTATGATACC 266
XX
QY 97 GTGACCTCGAGGGGGGCTTAACCTAATTTGTT 134
DB 267 GTGACCTCGAGGGGGGCTTAACCTAATTTGTT 304
XX
RESULT 14
ABV36219
ID ABV36219 standard; cDNA; 380 BP.
XX
AC ABV36219;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 36210.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.

```
PR 13-DEC-2000; 2000US-255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA Schlegel R, Endege WO, Monahan JE;
XX WPI: 2001-662795/76.
DR
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 7497; 11750pp; English.
CC
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 380 BP; 106 A; 89 C; 93 G; 92 T; 0 other;

Query Match          49.7%; Score 74; DB 23; Length 380;
Best Local Similarity 73.1%; Pred. No. 1.5e-15;
Matches 95; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 5 AAAAAATTGAAACTAGATCTATTATTGCAAGCGCGGCCCATGATGATCCCGGGGC 64
DB 103 ACAATTTATAGTTAATACGAAAGTTACCGCTAGAACTAGTGGATCCCGGGGC 162
QY 65 TGCAGGAAATTCGATATCAAGCTTATCGATACCGTCGAGCGGGGGCCCTAACTAAC 124
DB 163 TGCAGGAAATTCGATATCAAGCTTATCGATACCGTCGAGCGGGGGCCCGGTACCC 222
QY 125 TAATTTGTT 134
DB 223 AGCTTTGTT 232

RESULT 15
ABV45265
ID ABV45265 standard; cDNA; 380 BP.
XX
AC ABV45265;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 45256.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN MO200160860-A2.
PD
XX 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
```

```
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA Schlegel R, Endege WO, Monahan JE;
XX WPI: 2001-662795/76.
DR
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 8960; 11750pp; English.
CC
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 380 BP; 106 A; 89 C; 93 G; 92 T; 0 other;

Query Match          49.7%; Score 74; DB 23; Length 380;
Best Local Similarity 73.1%; Pred. No. 1.5e-15;
Matches 95; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 5 AAAAAATTGAAACTAGATCTATTATTGCAAGCGCGGCCCATGATGATCCCGGGGC 64
DB 103 ACAATTTATAGTTAATACGAAAGTTACCGCTAGAACTAGTGGATCCCGGGGC 162
QY 65 TGCAGGAAATTCGATATCAAGCTTATCGATACCGTCGAGCGGGGGCCCTAACTAAC 124
DB 163 TGCAGGAAATTCGATATCAAGCTTATCGATACCGTCGAGCGGGGGCCCGGTACCC 222
QY 125 TAATTTGTT 134
DB 223 AGCTTTGTT 232
```

Search completed: November 10, 2002, 05:58:28
Job time : 175.807 secs


```

; APPLICANT: University of Rochester
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
; FILE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells
; FILE REFERENCE: 1821.0070004
; CURRENT APPLICATION NUMBER: US/09/987,456
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/271,424
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/262,067
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/298,087
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/249,268
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin version 3.1
; LENGTH: 149
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: p7.5/ATG2/lk vector
US-09-987-456-4
Query Match          100.0%; Score 149; DB 10; Length 149;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY 1 GGGCAAAATTTGAAAATCTATTTATTTGACGCGCGCCCATGAGTGCATCCCC 60
    |||||||
DB 1 GGGCAAAATTTGAAAATCTATTTATTTGACGCGCGCCCATGAGTGCATCCCC 60
QY 61 GGGCTGACGAATTCGATCAACGCTTATGATACGCTGCACCTCGAGGGGGGCTAAC 120
    |||||||
DB 61 GGGCTGACGAATTCGATCAACGCTTATGATACGCTGCACCTCGAGGGGGGCTAAC 120
QY 121 TAACTAATTTGTTTGTGGCGCCGGCC 149
    |||||||
DB 121 TAACTAATTTGTTTGTGGCGCCGGCC 149
```

```

RESULT 3
; Sequence 9, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
; CURRENT APPLICATION NUMBER: US/09/822,250
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 9
; LENGTH: 150
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-822-250-9
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Query Match          92.6%; Score 138; DB 10; Length 150;
Best Local Similarity 99.3%; Pred. No. 1.6e-42;
Matches 149; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 GGGCAAAATTTGAAAATCTATTTATTTGACGCGCGCCCATGAGTGCATCCCC 59
    |||||||
DB 1 GGGCAAAATTTGAAAATCTATTTATTTGACGCGCGCCCATGAGTGCATCCCC 60
QY 60 CGGCTGACGAATTCGATCAACGCTTATGATACGCTGCACCTCGAGGGGGGCTTAA 119
    |||||||
```

```

DB 61 CGGCTGACGAATTCGATCAACGCTTATGATACGCTGCACCTCGAGGGGGGCTTAA 120
QY 120 CTAACATAATTTGTTTGTGGCGCCGGCC 149
    |||||||
DB 121 CTAACATAATTTGTTTGTGGCGCCGGCC 150
```

```

RESULT 4
US-09-987-456-5
; Sequence 5, Application US/09987456
; Patent No. US20020123057A1
; GENERAL INFORMATION:
; APPLICANT: University of Rochester
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
; FILE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells
; FILE REFERENCE: 1821.0070004
; CURRENT APPLICATION NUMBER: US/09/987,456
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/271,424
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/262,067
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/298,087
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/249,268
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 150
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: p7.5/ATG3/lk vector
US-09-987-456-5
```

```

Query Match          92.6%; Score 138; DB 10; Length 150;
Best Local Similarity 99.3%; Pred. No. 1.6e-42;
Matches 149; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 GGGCAAAATTTGAAAATCTAGATCTATTTATTTGACGCGCGCCCATGAGTGCATCC 59
    |||||||
DB 1 GGGCAAAATTTGAAAATCTAGATCTATTTATTTGACGCGCGCCCATGAGTGCATCC 60
QY 60 CGGCTGACGAATTCGATCAACGCTTATGATACGCTGCACCTCGAGGGGGGCTTAA 119
    |||||||
DB 61 CGGCTGACGAATTCGATCAACGCTTATGATACGCTGCACCTCGAGGGGGGCTTAA 120
QY 120 CTAACATAATTTGTTTGTGGCGCCGGCC 149
    |||||||
DB 121 CTAACATAATTTGTTTGTGGCGCCGGCC 150
```

```

RESULT 5
US-09-822-250-7
; Sequence 7, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
; CURRENT APPLICATION NUMBER: US/09/822,250
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 148
; TYPE: DNA
; ORGANISM: synthetic construct
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QY	121 TAACATAATTTGTTTTGTGGCCCGGCC	149
Db	117 TAACATAATTTGTTTTGTGGCCCGGCC	145

```

RESULT 9
US-09-834-975-601/C
; Sequence 601, Application US/09834975
; Patent No. US20020110815A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Brown, Jeffrey
; APPLICANT: Bolt, Andrew
; APPLICANT: Van Hufel, Christophe
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; FILE REFERENCE: MRI-016B
; CURRENT APPLICATION NUMBER: US/09/834,975
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,538
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 1046
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 601
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-975-601

```

	Query Match	47.0%;	Score 70;	DB 10;	Length 424;
	Best Local Similarity	88.4%;	Pred. No. 8.8e-17;		
	Matches 76;	Conservative 0;	Mismatches 10;	Indels 0;	Gaps 0;
QY	49 AATGATATCCCCGGGCTGAGAGAAATTCATATCAACGTTATCGATACCTCGACCTCGAG	108			
DB	105 AATGATATCCCCGGGCTGAGAGAAATTCATATCAACGTTATCGATACCTCGACCTCGAG	46			
QY	109 GGGGGGCTTAATACTAATTTGTT	134			
DB	45 GGGGGGCTTAATACTAATTTGTT	20			

```

1  RESULT 10
2  ; Sequence 91, Application US/09735705
3  ; Patent No. US2002005329A1
4  ; GENERAL INFORMATION:
5  ; APPLICANT: Wang, Tonglong
6  ; APPLICANT: Fan, Liqun
7  ; APPLICANT: Kalos, Michael D.
8  ; APPLICANT: Bangur, Chaitanya S.
9  ; APPLICANT: Hosken, Nancy
10 ; APPLICANT: Fanger, Gary R.
11 ; APPLICANT: Li, Samuel X.
12 ; APPLICANT: Wang, Aijun
13 ; APPLICANT: Skeiky, Yasir A.W.
14 ; APPLICANT: Henderson, Robert A.
15 ; APPLICANT: McNeill, Patricia D.
16 ; APPLICANT: Fanger, Neil
17 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
18 ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
19 ; FILE REFERENCE: 210121.455C14
20 ; CURRENT APPLICATION NUMBER: US/09/735,705
21 ; CURRENT FILING DATE: 2000-12-12
22 ; NUMBER OF SEQ ID NOS: 419
23 ; SOFTWARE: FastSeq for Windows Version 3.0
24 ; SEQ ID NO 91
25 ; LENGTH: 858
26 ; TYPE: DNA
27 ; ORGANISM: Homo sapien
28 ; FEATURE:

```

```

; NAME/KEY: misc_feature
; LOCATION: (1)..(858)
; OTHER INFORMATION: n = A,T,C or G
US-09-735-705-91

```

[illegible]

```

RESULT 11
US-09-850-716A-91
; Sequence 91, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ. ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 91
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(858)
; OTHER INFORMATION: n = A,T,C or G
US-09-850-716A-91

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Query Match	46.6%;	Score 69.4;	DB 10;	Length 858;
Best Local Similarity	76.6%;	Pred. No. 2e-16;		
Matches	85;	Conservative	0;	Mismatches 26;
			Indels	0;
			Gaps	0

QY 6 AAATTTGAAAACTGATCTATTATTTCACAGGGGCGCCATGAGTGTATCCCCGGGCT 65
Db 313 ATTAATCTCACCGAGGATTCACAGATTCACACACATCTGGACTGTGTGATGCCCGGGCT 372
QY 66 GCAGGAATTCGATCAAGCTTATTGATACCGTCGACCTCGAGGGGGGCC 116
Db 373 GCAGGAATTCGATCAAGCTTATTGATACCGTCGACCTCGAGGGGGGCC 423

```

RESULT 12 778-91
; Sequence 91, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Cartick, Derrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LONG CANCER
; FILE REFERENCE: 210121.455C16

```

```
;; CURRENT APPLICATION NUMBER: US/09/897,778
;; CURRENT FILING DATE: 2001-06-28
;; NUMBER OF SEQ ID NOS: 467
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 91
;; LENGTH: 858
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 570, 591, 655, 664, 667, 683, 711, 759, 760, 765, 777, 787,
;; LOCATION: 792, 794, 801, 804, 809, 817, 820
;; OTHER INFORMATION: n = A,T,C or G
US-09-897-778-91
```

```
Query Match
Best Local Similarity 46.0%; Score 69.4; DB 10; Length 858;
Matches 85; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
```

```
QY 6 AAAATTGAAACTAGATCTATTATTGACGGCGCCGCCAATGATGATCCCGGGGCT 65
DB 313 ATATATCTCACGAGNATTCACGATTCACACACTGACTAGTGGATCCCGGGGCT 372
QY 66 GCAGGATTCGATATCACTTATCGATACCGTGCACCTCGAGGGGGGCC 116
DB 373 GCAGGATTCGATATCACTTATCGATACCGTGCACCTCGAGGGGGGCC 423
```

RESULT 13

```
;; Sequence 306, Application US/09735705
;; Patent No. US20020052329A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, Tonglong
;; APPLICANT: Fan, Liqun
;; APPLICANT: Kalos, Michael D.
;; APPLICANT: Bangur, Chaitanya S.
;; APPLICANT: Hosken, Nancy
;; APPLICANT: Fanger, Gary R.
;; APPLICANT: Li, Samuel X.
;; APPLICANT: Wang, Aljun
;; APPLICANT: Skelky, Yasir A.W.
;; APPLICANT: Henderson, Robert A.
;; APPLICANT: McNeill, Patricia D.
;; APPLICANT: Fanger, Neil
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;; FILE REFERENCE: 210121.455C14
;; CURRENT APPLICATION NUMBER: US/09/735,705
;; CURRENT FILING DATE: 2000-12-12
;; NUMBER OF SEQ ID NOS: 419
;; SOFTWARE: FASTSEQ for Windows Version 3.0
;; SEQ ID NO 306
;; LENGTH: 457
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-09-735-705-306
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```
Query Match
Best Local Similarity 46.0%; Score 68.6; DB 10; Length 457;
Matches 71; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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```
QY 42 CGCCATGATGATGATCCCGGGCTGCAGAAATTCATATCAAGTTATGATACCGTGA 101
DB 352 CACAACTAGTGTGATCCCGGGCTGCAGAAATTCATATCAAGTTATGATACCGTGA 411
QY 102 CCTCGAGGGGGGCC 116
DB 412 CCTCGAGGGGGGCC 426
```

RESULT 14

US-09-850-716A-306

```
;; Sequence 306, Application US/09850716A
;; Patent No. US20020115139A1
;; GENERAL INFORMATION:
;; APPLICANT: Kalos, Michael D.
;; APPLICANT: McNeill, Patricia D.
;; APPLICANT: Retter, Marc W.
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;; FILE REFERENCE: 210121.455C15
;; CURRENT APPLICATION NUMBER: US/09/850,716A
;; CURRENT FILING DATE: 2001-05-07
;; NUMBER OF SEQ ID NOS: 440
;; SOFTWARE: FASTSEQ for Windows Version 3.0
;; SEQ ID NO 306
;; LENGTH: 457
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-09-850-716A-306
```

```
Query Match
Best Local Similarity 46.0%; Score 68.6; DB 10; Length 457;
Matches 71; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 42 CGCCATGATGATGATCCCGGGCTGCAGAAATTCATATCAAGTTATGATACCGTGA 101
DB 352 CACAACTAGTGTGATCCCGGGCTGCAGAAATTCATATCAAGTTATGATACCGTGA 411
QY 102 CCTCGAGGGGGGCC 116
DB 412 CCTCGAGGGGGGCC 426
```

RESULT 15

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;; US-09-897-778-306
;; Sequence 306, Application US/09897778
;; Patent No. US20020147143A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, Tonglong
;; APPLICANT: Marnierakis, Margarita
;; APPLICANT: Fanger, Gary R.
;; APPLICANT: Vedvick, Thomas S.
;; APPLICANT: Carter, Darick
;; APPLICANT: Watanabe, Yoshihiro
;; APPLICANT: Henderson, Robert A.
;; APPLICANT: Peckham, David W.
;; APPLICANT: Fanger, Neil
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;; FILE REFERENCE: 210121.455C16
;; CURRENT APPLICATION NUMBER: US/09/897,778
;; CURRENT FILING DATE: 2001-06-28
;; NUMBER OF SEQ ID NOS: 467
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 306
;; LENGTH: 457
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-897-778-306
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Query Match
Best Local Similarity 46.0%; Score 68.6; DB 10; Length 457;
Matches 71; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 42 CGCCATGATGATGATCCCGGGCTGCAGAAATTCATATCAAGTTATGATACCGTGA 101
DB 352 CACAACTAGTGTGATCCCGGGCTGCAGAAATTCATATCAAGTTATGATACCGTGA 411
QY 102 CCTCGAGGGGGGCC 116
DB 412 CCTCGAGGGGGGCC 426
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Search completed: November 10, 2002, 11:33:46

Tue Nov 12 06:25:43 2002

us-08-935-377-8.rnpb

Page 6

Job time : 37.0825 secs

FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 306
LENGTH: 457
TYPE: DNA
ORGANISM: Homo sapien
US-09-643-597-306

Query Match
Best Local Similarity 94.7%; Score 68.6; DB 4; Length 457;
Matches 71; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 42 CGCGATGATGATCCCGGCTGCAGGATTCGATATCAAGCTTATGATACCGTCGA 101
DB 352 CACACTAGTAGATCCCGGCTGCAGGATTCGATATCAAGCTTATGATACCGTCGA 411
QY 102 CCTCGAGGGGGGCC 116
DB 412 CCTCGAGGGGGGCC 426

RESULT 5
US-09-323-872A-26/c
Sequence 26, Application US/09323872A
Patent No. 6395539
GENERAL INFORMATION:
APPLICANT: Coschignano, Peter
TITLE OF INVENTION: Compositions and Methods for Bioremediation
FILE REFERENCE: OHU-03640
CURRENT APPLICATION NUMBER: US/09/323,872A
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 09/072,433
PRIOR FILING DATE: 1998-05-04
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn version 3.0
SEQ ID NO 26
LENGTH: 147
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(147)
US-09-323-872A-26

Query Match
Best Local Similarity 100.0%; Score 68; DB 4; Length 147;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 AGTGATCCCGGCTGCAGGATTCGATATCAAGCTTATGATACCGTCGAG 108
DB 107 AGTGATCCCGGCTGCAGGATTCGATATCAAGCTTATGATACCGTCGAG 48

QY 109 GGGGGGCC 116
DB 47 GGGGGGCC 40

RESULT 6
US-08-976-259-108/c
Sequence 108, Application US/08976259
Patent No. 6316609
GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Choi, Gil H.
APPLICANT: Welch, Rodney A.
TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli
PATENT NO. 6316609
NUMBER OF SEQUENCES: 142
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Ave, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,259
FILING DATE: Herewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,626 AND US 60/061,953
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488, 0740002/EKS/CBM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-976-259-108

Query Match
Best Local Similarity 100.0%; Score 68; DB 4; Length 752;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 AGTGATCCCGGCTGCAGGATTCGATATCAAGCTTATGATACCGTCGAG 108
DB 73 AGTGATCCCGGCTGCAGGATTCGATATCAAGCTTATGATACCGTCGAG 14
QY 109 GGGGGGCC 116
DB 13 GGGGGGCC 6

RESULT 7
US-08-446-935-6/c
Sequence 6, Application US/08446935
Patent No. 6187991
GENERAL INFORMATION:
APPLICANT: Soeller, Walter C.
APPLICANT: Carly, Maynard D.
APPLICANT: Kreutler, David K.
TITLE OF INVENTION: TRANSGENIC ANIMAL MODELS FOR TYPE II
TITLE OF INVENTION: DIABETES MELLITUS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pfizer Inc.
STREET: 235 East 42nd Street, 20th Floor
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10017-5755
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,935
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sheyka, Robert F.

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;
;   REGISTRATION NUMBER: 31,304
;   REFERENCE/DOCKET NUMBER: PC8153
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212)573-1189
;   TELEFAX: (212)573-1939
;   TELEX: N/A
;   INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 2961 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: circular
;   MOLECULE TYPE: DNA (genomic)
;
US-08-446-935-6

Query Match
Best Local Similarity 45.6%; Score 68; DB 4; Length 2961;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 AGTGATCCCCCGGCTGCAGATTCGATTCAGCTTATCGTACCGCTCGAG 108
DB 727 AGTGATCCCCCGGCTGCAGATTCGATTCAGCTTATCGTACCGCTCGAG 668
QY 109 GGGGGGCC 116
DB 667 GGGGGGCC 660

RESULT 8
US-08-992-334-1/C
; Sequence 1, Application US/08992334
; Patent No. 5919678
;
GENERAL INFORMATION:
; APPLICANT: Gruss, Alexandra
; APPLICANT: Maguin, Emmanuelle
; TITLE OF INVENTION: METHODS FOR USING A TEMPERATURE-SENSITIVE
; TITLE OF INVENTION: PLASMID
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christie Parker & Hale, LLP
; STREET: 350 West Colorado Boulevard, Suite 500
; CITY: Pasadena
; STATE: California
; COUNTRY: United States
; ZIP: 91105
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/992,334
; FILING DATE: 17-DEC-1997
; CLASSIFICATION: 435
;
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/302,752
; FILING DATE: 24-DEC-1994
;
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR93/00248
; FILING DATE: 12-MAR-1993
;
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/03034
; FILING DATE: 13-MAR-1992
;
ATTORNEY/AGENT INFORMATION:
; NAME: Prout, D. Bruce
; REGISTRATION NUMBER: 20958
; REFERENCE/DOCKET NUMBER: C93:31779
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 795-9900
; TELEFAX: (626) 577-8800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3792 base pairs
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;   TYPE: nucleic acid
;   STRANDEDNESS: both
;   TOPOLOGY: circular
;   MOLECULE TYPE: DNA (genomic)
;   HYPOTHETICAL: NO
;   ANTI-SENSE: YES
;   IMMEDIATE SOURCE:
;   CLONE: pg+host4
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US-08-992-334-1

Query Match
Best Local Similarity 45.6%; Score 68; DB 2; Length 3792;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 3542 AGTGATCCCCCGGCTGCAGATTCGATTCAGCTTATCGATACCGCTCGAG 3483
QY 109 GGGGGGCC 116
DB 3482 GGGGGGCC 3475

RESULT 9
US-08-302-752-1/C
; Sequence 1, Application US/08302752
; Patent No. 6025190
;
GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THERMOSENSIBLE PLASMID
; NUMBER OF SEQUENCES: 3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,752
; FILING DATE:
; CLASSIFICATION: 435
;
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9203034
; FILING DATE: 13-MAR-1992
;
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR/93/00248
; FILING DATE: 12-MAR-1993
;
INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3792 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-302-752-1

Query Match
Best Local Similarity 45.6%; Score 68; DB 3; Length 3792;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 3542 AGTGATCCCCCGGCTGCAGATTCGATTCAGCTTATCGATACCGCTCGAG 3483
QY 109 GGGGGGCC 116
DB 3482 GGGGGGCC 3475

RESULT 10
US-08-410-540-3
; Sequence 3, Application US/08410540
; Patent No. 5807678
;
GENERAL INFORMATION:
```


APPLICANT: Miller, Walter L.
APPLICANT: Lin, Dong
APPLICANT: Straus III, Jerome F.
TITLE OF INVENTION: IDENTIFICATION OF GENE MUTATIONS
TITLE OF INVENTION: ASSOCIATED WITH CONGENITAL LIPOID ADRENAL HYPERPLASIA
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,540
FILING DATE: 23-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard L.
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-238/000S
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 853 5070
TELEFAX: 415 857 0663
TELEX: 380816COOLEYPA
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4016 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: exon
LOCATION: 1098..1283
FEATURE:
NAME/KEY: exon
LOCATION: 1620..1733
FEATURE:
NAME/KEY: exon
LOCATION: 2047..2174
FEATURE:
NAME/KEY: exon
LOCATION: 2267..2425
FEATURE:
NAME/KEY: exon
LOCATION: 2567..2751
FEATURE:
NAME/KEY: exon
LOCATION: 2828..2921
FEATURE:
NAME/KEY: exon
LOCATION: 3031..3765
FEATURE:
NAME/KEY: 1433..1434
OTHER INFORMATION: /note= "interruption of sequence data"
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NAME/KEY: 2208..2209
OTHER INFORMATION: /note= "interruption of sequence data"
FEATURE:
NAME/KEY: 2781..2782
OTHER INFORMATION: /note= "interruption of sequence data"
FEATURE:

NAME/KEY: -
LOCATION: 2956..2957
OTHER INFORMATION: /note= "interruption of sequence data"
US-08-410-540-3
Query Match
Best Local Similarity 45.6%; Score 68; DB 1; Length 4016;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 49 AGTGATCCCCGGCGTCGAGATTCGATATCAAGCTTATCGATTACCGTCGACCTGAG 108
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DB 3938 AGTGATCCCCGGCGTCGAGATTCGATATCAAGCTTATCGATTACCGTCGACCTGAG 3997
QY 109 GGGGGGCC 116
|||||
DB 3998 GGGGGGCC 4005

RESULT 11
US-08-992-334-2/c
Sequence 2, Application US/08992334
Patent No. 5919678
GENERAL INFORMATION:
APPLICANT: Gruss, Alexandra
APPLICANT: Maguid, Emmanuelle
TITLE OF INVENTION: METHODS FOR USING A TEMPERATURE-SENSITIVE
TITLE OF INVENTION: PLASMID
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christie Parker & Hale, LLP
STREET: 350 West Colorado Boulevard, Suite 500
CITY: Pasadena
STATE: California
COUNTRY: United States
ZIP: 91105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/992,334
FILING DATE: 17-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,752
FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00248
FILING DATE: 12-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 992/03034
FILING DATE: 13-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Proulx, D. Bruce
REGISTRATION NUMBER: 20958
REFERENCE/DOCKET NUMBER: C93:31779
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 795-9900
TELEFAX: (626) 577-8800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5234 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
US-08-992-334-2

Query Match 45.6%; Score 68; DB 2; Length 5234;
Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      49  AGTGAATCCCCGGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTGCAGCTCGAG  108
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Db      4984  AGTGAATCCCCGGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTGCAGCTCGAG  4925

QY      109  GGGGGGCC  116
          |||||||
Db      4924  GGGGGGCC  4917

RESULT  12
US-08-302-752-2/c
; Sequence 2, Application US/08302752
Patent No. 6025190
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: THERMOSENSIBLE PLASMID
NUMBER OF SEQUENCES: 3
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,752
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9203034
FILING DATE: 13-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR/93/00248
FILING DATE: 12-MAR-1993
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-302-752-2

Query Match      45.6%; Score 68; DB 3; Length 5234;
Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY      49  AGTGAATCCCCGGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTGCAGCTCGAG  108
          |||||||
Db      4984  AGTGAATCCCCGGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTGCAGCTCGAG  4925

QY      109  GGGGGGCC  116
          |||||||
Db      4924  GGGGGGCC  4917

RESULT  13
US-09-495-797-37
; Sequence 37, Application US/09495797
Patent No. 6369296
GENERAL INFORMATION:
APPLICANT: Ratcliff, Frank G
APPLICANT: Martin-Hernandez, Ana M
APPLICANT: Baulcombe, David C
TITLE OF INVENTION: Viral Vectors
FILE REFERENCE: Mewburn 43,047
CURRENT APPLICATION NUMBER: US/09/495,797
CURRENT FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn version 3.0
SEQ ID NO 37
LENGTH: 5592
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

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; OTHER INFORMATION: PT000
US-09-495-797-37

Query Match      45.6%; Score 68; DB 4; Length 5592;
Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY    49 AGTGATCCCCGGGCTCAGGAATTGCATTCACAGTTTATCGATTACCGTCGACTCGAG 108
Db    2550 ACTGATATCCCCGGGCTCAGGAATTGCATTCACAGTTTATCGATTACCGTCGACTCGAG 2609
OY    109 GGGGGGCC 116
Db    2610 GGGGGGCC 2617

RESULT 14
US-08-992-334-3/c
; Sequence 3, Application US/08992334
; Patent No. 5919678
; GENERAL INFORMATION:
; APPLICANT: Gruss, Alexandra
; APPLICANT: Maguin, Emmanuelle
; TITLE OF INVENTION: METHODS FOR USING A TEMPERATURE-SENSITIVE
; TITLE OF INVENTION: PLASMD
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christie Parker & Hale, LLP
; STREET: 350 West Colorado Boulevard, Suite 500
; CITY: Pasadena
; STATE: California
; COUNTRY: United States
; ZIP: 91105

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/992,334
; APPLICATION NUMBER: US/08/992,334
; FILING DATE: 17-DEC-1997
; CLASSIFICATION: 435
; APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 08/302,752
; FILING DATE: 24-DEC-1994
; APPLICATION DATA:
; PRIOR APPLICATION DATA: PCT/FR93/00248
; FILING DATE: 12-MAR-1993
; APPLICATION DATA:
; PRIOR APPLICATION NUMBER: FR 892/03034
; FILING DATE: 13-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Prout, D. Bruce
; REGISTRATION NUMBER: 20958
; REFERENCE/DOCKET NUMBER: C93:31779
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 795-9900
; TELEFAX: (626) 577-8800
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6722 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; US-08-992-334-3

Query Match      45.6%; Score 68; DB 2; Length 6722;
Best Local Similarity 100.0%; Pred. No. 2.1e-14;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY    49 AGTGATCCCCGGGCTCAGGAATTGCATTCACAGTTTATCGATTACCGTCGACTCGAG 108

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DB 6472 AGTGGATCCCCGGGCGTGCAGGATTGCATATCAAGCTTATCGATACCGTCGACCTCGAG 6413
QY 109 GGGGGGCC 116
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DB 6412 GGGGGGCC 6405

RESULT 15
US-08-302-752-3/c
; Sequence 3, Application US/08302752
; Patent No. 6025190
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THERMOSENSIBLE PLASMID
; NUMBER OF SEQUENCES: 3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA: US/08/302,752
; APPLICATION NUMBER: US/08/302,752
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9203034
; FILING DATE: 13-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR/93/00248
; FILING DATE: 12-MAR-1993
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6722 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-302-752-3

Query Match 45.68; Score 68; DB 3; Length 6722;
Best Local Similarity 100.0%; Pred. No. 2.1e-14;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 49 ACTGATCCCCGGGCGTGCAGGATTGCATATCAAGCTTATCGATACCGTCGACCTCGAG 108
|||||||
DB 6472 AGTGGATCCCCGGGCGTGCAGGATTGCATATCAAGCTTATCGATACCGTCGACCTCGAG 6413
QY 109 GGGGGGCC 116
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DB 6412 GGGGGGCC 6405

Search completed: November 10, 2002, 08:36:20
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:05:45 ; Search time 729.31 Seconds

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Title: US-08-935-377-9

Sequence: 1 GGGCAAAATGAAAACTA.....TTGTTTGTGGGCGCGCC 150

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: gb_pr:*
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11: gb_sts:*
12: gb_sy:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	138	92.0	149	6 AX326745	AX326745 Sequence
3	136	90.7	148	6 AX326744	AX326744 Sequence
4	130	86.7	145	6 AX326743	AX326743 Sequence
5	72.2	48.1	855	6 AX461060	AX461060 Sequence
6	69.8	46.5	793	6 AR060142	AR060142 Sequence
7	69.8	46.5	793	6 AR087297	AR087297 Sequence
8	69.8	46.5	793	6 AR134484	AR134484 Sequence
9	69.8	46.5	793	6 AR144585	AR144585 Sequence
10	69.8	46.5	13558	6 AX287041	AX287041 Sequence
11	69	46.0	259	6 A44281	A44281 Sequence 9
12	69	46.0	424	6 AX284796	AX284796 Sequence
13	69	46.0	2059	12 AY034154	AY034154 Cloning v
14	69	46.0	2890	9 AB035274	AB035274 Homo sap1
15	69	46.0	2958	6 AX247548	AX247548 Sequence
16	69	46.0	2958	12 ARBLKSM	ARBLKSM
17	69	46.0	2958	12 ARBLKSP	ARBLKSP
18	69	46.0	2961	12 ARBL2KSM	ARBL2KSM
19	69	46.0	2961	12 ARBL2KSP	ARBL2KSP
20	69	46.0	2964	12 SYNBLKSMV	SYNBLKSMV
21	69	46.0	2964	12 SYNBLKSPV	SYNBLKSPV
22	69	46.0	3306	12 SYNBLKSM6	SYNBLKSM6
23	69	46.0	3417	12 AF153422	AF153422 Cloning v
24	69	46.0	3485	12 AF178449	AF178449 Integrati
25	69	46.0	4144	12 XXU35131	XXU35131 Plasmid PBS
26	69	46.0	4267	12 PRS304	PRS304
27	69	46.0	4289	12 XXU35136	XXU35136
28	69	46.0	4373	12 PRS306	PRS306
29	69	46.0	4443	12 PRS303	PRS303
30	69	46.0	4549	12 AF178452	AF178452
31	69	46.0	4670	12 ASAJ5326	ASAJ5326 pgAI(+)
32	69	46.0	4670	12 ASAJ5329	ASAJ5329 pgAI(-)
33	69	46.0	4707	12 XXU02374	XXU02374
34	69	46.0	4768	12 XXU25061	XXU25061
35	69	46.0	4783	12 PRS314	PRS314
36	69	46.0	4887	12 PRS316	PRS316
37	69	46.0	4950	12 XXU25060	XXU25060
38	69	46.0	4967	12 PRS313	PRS313
39	69	46.0	5144	12 CVU23751	CVU23751
40	69	46.0	5187	12 U34887	U34887
41	69	46.0	5228	12 XXU25059	XXU25059
42	69	46.0	5504	12 PRS305	PRS305
43	69	46.0	5634	12 CVU14125	CVU14125
44	69	46.0	5973	12 AF504908	AF504908 Cloning v
45	69	46.0	6018	12 PRS315	PRS315

ALIGNMENTS

RESULT 1
AX326746 LOCUS 150 bp
DEFINITION Sequence 7 from Patent WO0172995.
ACCESSION AX326746
VERSION AX326746.1 GI:18097472
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Zauderer, M. and Smith, E. S.
TITLE Methods of producing a library and methods of selecting polynucleotides of interest
JOURNAL Patent: WO 01/72995-A 7 04-OCT-2001.

UNIVERSITY OF ROCHESTER (US)
Location/Qualifiers
1. 150
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Nucleotide Sequence of p7.5/ATG3/tk"

BASE COUNT 36 a 38 c 39 g 37 t

ORIGIN

Query Match 100.0%; Score 150; DB 6; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.6e-38;
Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCCAAAATTGAAAATCTAGATCTATTATTGACGCGCGCCGACATGATGATCCCC 60
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Db 1 GGCCAAAATTGAAAATCTAGATCTATTATTGACGCGCGCCGACATGATGATCCCC 60

QY 61 CGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTGCACCTCGAGGGGGGCGCTAA 120
|||||
Db 61 CGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTGCACCTCGAGGGGGGCGCTAA 120

QY 121 CTAACATAATTTGTTTTGTTGGCGCCGCC 150
|||||
Db 121 CTAACATAATTTGTTTTGTTGGCGCCGCC 150

RESULT 2
AX326745 149 bp DNA linear PAT 07-JAN-2002
LOCUS
DEFINITION Sequence 6 from Patent WO0172995.
ACCESSION AX326745
VERSION AX326745.1 GI:18097471
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Zauderer,M. and Smith,E.S.
TITLE Methods of producing a library and methods of selecting polynucleotides of interest
JOURNAL Patent: WO 0172995-A 6 04-OCT-2001;
UNIVERSITY OF ROCHESTER (US)
FEATURES
source 1. 149
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Nucleotide Sequence of p7.5/ATG3/tk"

BASE COUNT 36 a 37 c 39 g 37 t

ORIGIN

Query Match 92.0%; Score 138; DB 6; Length 149;
Best Local Similarity 99.3%; Pred. No. 1.4e-34;
Matches 149; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGCCAAAATTGAAAATCTAGATCTATTATTGACGCGCGCCGACATGATGATCCCC 60
|||||
Db 1 GGCCAAAATTGAAAATCTAGATCTATTATTGACGCGCGCCGACATGATGATCCCC 59

QY 61 CGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTGCACCTCGAGGGGGGCGCTAA 120
|||||
Db 61 CGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTGCACCTCGAGGGGGGCGCTAA 119

QY 121 CTAACATAATTTGTTTTGTTGGCGCCGCC 150
|||||
Db 120 CTAACATAATTTGTTTTGTTGGCGCCGCC 149

RESULT 3
AX326744 148 bp DNA linear PAT 07-JAN-2002
LOCUS
DEFINITION Sequence 5 from Patent WO0172995.
ACCESSION AX326744
VERSION AX326744.1 GI:18097470

KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Zauderer,M. and Smith,E.S.
TITLE Methods of producing a library and methods of selecting polynucleotides of interest
JOURNAL Patent: WO 0172995-A 5 04-OCT-2001;
UNIVERSITY OF ROCHESTER (US)
FEATURES
source 1. 148
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Nucleotide Sequence of p7.5/ATG1/tk"

BASE COUNT 35 a 37 c 39 g 37 t

ORIGIN

Query Match 90.7%; Score 136; DB 6; Length 148;
Best Local Similarity 98.7%; Pred. No. 6.4e-34;
Matches 148; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 GGCCAAAATTGAAAATCTAGATCTATTATTGACGCGCGCCGACATGATGATCCCC 60
|||||
Db 1 GGCCAAAATTGAAAATCTAGATCTATTATTGACGCGCGCCGACATGATGATCCCC 58

QY 61 CGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTGCACCTCGAGGGGGGCGCTAA 120
|||||
Db 59 CGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTGCACCTCGAGGGGGGCGCTAA 118

QY 121 CTAACATAATTTGTTTTGTTGGCGCCGCC 150
|||||
Db 119 CTAACATAATTTGTTTTGTTGGCGCCGCC 148

RESULT 4
AX326743 145 bp DNA linear PAT 07-JAN-2002
LOCUS
DEFINITION Sequence 4 from Patent WO0172995.
ACCESSION AX326743
VERSION AX326743.1 GI:18097469
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Zauderer,M. and Smith,E.S.
TITLE Methods of producing a library and methods of selecting polynucleotides of interest
JOURNAL Patent: WO 0172995-A 4 04-OCT-2001;
UNIVERSITY OF ROCHESTER (US)
FEATURES
source 1. 145
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Nucleotide Sequence of p7.5/ATG0/tk"

BASE COUNT 34 a 37 c 38 g 36 t

ORIGIN

Query Match 86.7%; Score 130; DB 6; Length 145;
Best Local Similarity 96.7%; Pred. No. 6e-32;
Matches 145; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 GGCCAAAATTGAAAATCTAGATCTATTATTGACGCGCGCCGACATGATGATCCCC 60
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Db 1 GGCCAAAATTGAAAATCTAGATCTATTATTGACGCGCGCGC-----CGTGAATCCCC 55

QY 61 CGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTGCACCTCGAGGGGGGCGCTAA 120
|||||
Db 56 CGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTGCACCTCGAGGGGGGCGCTAA 115

QY 121 CTAACATAATTTGTTTTGTTGGCGCCGCC 150
|||||

ACCESSION ARI44585
VERSION ARI44585.1 GI:15106452
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 793)
AUTHORS St. George-Hyslop, P.H., Remmens, J.M. and Fraser, P.E.
TITLE Genetic sequences and proteins related to Alzheimer's disease
JOURNAL Patent: US 6210919-A 121 03-APR-2001;
FEATURES
Source 1..793
/organism="unknown"
BASE COUNT 162 a 242 c 146 g 229 t 14 others
ORIGIN
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Best Local Similarity 82.5%; Pred. No. 5e-12;
Matches 80; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 39 GGGCGCCATGACGTGATCCCGGGCTGCAGGAATTCGATTCAGCTTATCGATACCG 98
DB 130 GGAGGCCCGGGCGGATCCCGGGCTGCAGGAATTCGATTCAGCTTATCGATACCG 71
QY 99 TCGACCTCGAGGGGGGCGCTACTACTAATTTTGT 135
DB 70 TCGACCTCGAGGGGGGCGGCTACCGACTTTTGT 34
RESULT 10
AX287041 13558 bp DNA linear PAT 21-NOV-2001
LOCUS AX287041
DEFINITION Sequence 5 from Patent WO0181623.
ACCESSION AX287041
VERSION AX287041.1 GI:17049037
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Goetz, B., Kammandel, B., Kuner, R., Scheek, S. and Hiemisch, H.
TITLE Novel neuronally expressed protein and use thereof
JOURNAL Patent: WO 0181623-A 5 01-NOV-2001;
FEATURES
Source 1..13558
Location/Qualifiers
/organism="Mus musculus"
/db_xref="taxon:10090"
BASE COUNT 2936 a 3419 c 3606 g 3544 t 53 others
ORIGIN
Query Match 46.5%; Score 69.8; DB 6; Length 13558;
Best Local Similarity 97.3%; Pred. No. 8.4e-12;
Matches 71; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 45 CARGAGCTGATCCCGGGCTGCAGGAATTCGATTCAGCTTATCGATACCGTGACG 104
DB 13481 CAGAGCTGATCCCGGGCTGCAGGAATTCGATTCAGCTTATCGATACCGTGACG 13540
QY 105 TCGAGGGGGGGCC 117
DB 13541 TCGAGGGGGGGCC 13553
RESULT 11
A44281 259 bp DNA linear PAT 07-MAR-1997
LOCUS A44281
DEFINITION Sequence 9 from Patent WO9511300.
ACCESSION A44281
VERSION A44281.1 GI:2299115
KEYWORDS
SOURCE unidentified.

ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 259)
AUTHORS Chandley, A.C., Kun, M., Sharkey, A.M., Hargreave, T.B. and Cooke, H.J.
JOURNAL AZOOSPERMIA IDENTIFICATION AND TREATMENT
COMMENT Patent: WO 9511300-A 9 27-APR-1995;
MEDICAL RES COUNCIL (GB)
Other publication AU 7947794 950508.
FEATURES
Source 1..259
/organism="unidentified"
/db_xref="taxon:32644"
/clone_11b="MOUSE GENOMIC LIBRARY"
BASE COUNT 67 a 58 c 63 g 69 t 2 others
ORIGIN
Query Match 46.0%; Score 69; DB 6; Length 259;
Best Local Similarity 88.2%; Pred. No. 7.5e-12;
Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 51 GTGATCCCGCGGCTGCAGGAATTCGATTCAGCTTATCGATACCGTCGACCTCGAGG 110
DB 112 GTGATCCCGCGGCTGCAGGAATTCGATTCAGCTTATCGATACCGTCGACCTCGAGG 53
QY 111 GGGGGCCTACTACTAATTTTGT 135
DB 52 GGGGGCCCGGTACCCAGCTTTTGT 28
RESULT 12
AX284796/c 424 bp DNA linear PAT 20-NOV-2001
LOCUS AX284796
DEFINITION Sequence 601 from Patent WO0179556.
ACCESSION AX284796
VERSION AX284796.1 GI:17045484
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Lillie, J., Brown, J.L., Bolt, A. and van Hufel, C.
TITLE Novel genes, compositions and methods for the identification,
assessment, prevention, and therapy of human cancers
JOURNAL Patent: WO 0179556-A 601 25-OCT-2001;
FEATURES
Source 1..424
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 87 a 134 c 118 g 85 t
ORIGIN
Query Match 46.0%; Score 69; DB 6; Length 424;
Best Local Similarity 88.2%; Pred. No. 8.2e-12;
Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 51 GTGATCCCGCGGCTGCAGGAATTCGATTCAGCTTATCGATACCGTCGACCTCGAGG 110
DB 104 GTGATCCCGCGGCTGCAGGAATTCGATTCAGCTTATCGATACCGTCGACCTCGAGG 45
QY 111 GGGGGCCTACTACTAATTTTGT 135
DB 44 GGGGGCCCGGTACCCAGCTTTTGT 20
RESULT 13
AY034154 2059 bp DNA circular SYN 23-JUL-2001
LOCUS AY034154/c
DEFINITION Cloning vector pIDN4, complete sequence.
ACCESSION AY034154
VERSION AY034154.1 GI:14324126

KEYWORDS Cloning vector pIDN4.
SOURCE Cloning vector pIDN4.
ORGANISM Artificial sequences; vectors.
REFERENCE 1 (bases 1 to 2059)
AUTHORS Hamilton,H.L., Schwartz,K.J. and Dillard,J.P.
TITLE Insertion-duplication mutagenesis of neisseria: use in
characterization of DNA transfer genes in the gonococcal genetic
island
JOURNAL J Bacteriol. 183 (16), 4718-4726 (2001)
MEDLINE 21359313
PUBMED 11466274
REFERENCE 2 (bases 1 to 2059)
AUTHORS Hamilton,H.L., Schwartz,K.J. and Dillard,J.P.
TITLE Direct Submision
JOURNAL Submitted (11-MAY-2001) Medical Microbiology & Immunology,
University of Wisconsin-Madison, 1300 University Avenue, Madison,
WI 53706, USA
FEATURES
source Location/Qualifiers
1..2059
/organism="Cloning vector pIDN4"
/db_xref="taxon:161273"
/note="for insertion-duplication mutagenesis in Neisseria"
40..59
/note="T3"
complement(187..204)
/note="T7"
277..311
complement(310..1113)
/gene="ermC"
complement(310..1044)
/gene="ermC"
/codon_start=1
/transl_table=11
/product="ErmC"
/protein_id="AAK58461.1"
/db_xref="GI:14324127"
/translation="MNEKIKHSQNTTSKHNIDKIMTINIRLNEDHNEIFSGKGF
TLELYORCNVTAIEIDHDKCTENKLVNDHNFQVLRNDILOFEPKNOYKIRGNI
PYNISTDILIRKIVFSDIADIELIVYGFARLRLNTKSLAFLAEYDISTSVPK
EYFHPKPVYSSLLRLNRKSRSHKDKQYVFWKWKKEKIKFTKQPNNSLKH
AGIDLNNTISFEQFLSLFNSYKLFNK"
complement(1051..1054)
/gene="ermC"
complement(1086..1091)
/gene="ermC"
complement(1108..1113)
/gene="ermC"
1130..1139
/note="DNA uptake sequence (DUS)"
complement(1145..1154)
/note="DNA uptake sequence (DUS)"
complement(1276..11976)
/note="RNA II"
complement(1422..1423)
1830..1835
1854..1859
1866..1973
/note="RNA I"
complement(1984..1989)
complement(2007..2012)
BASE COUNT 566 a 452 c 424 g 617 t
Query Match 46.0%; Score 69; DB 12; Length 2059;
Best Local Similarity 88.2%; Pred. No. 1.1e-11;
Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 51 GTGATCCCCCGGCTGCGAATTCGATATCAAGCTTATGATACCGTACCTCGAG 110
DB 143 GTGATCCCCCGGCTGCGAATTCGATATCAAGCTTATGATACCGTACCTCGAG 84
QY 111 GGGGCTACTACTAATTTGTT 135

Db 83 GGGGCGCGGTACCACTTTGTT 59
RESULT 14
AB035274
LOCUS
DEFINITION Homo sapiens mRNA for postreplication repair protein hRAD18p,
complete cds.
ACCESSION AB035274
VERSION AB035274.1 GI:8980616
KEYWORDS
SOURCE Homo sapiens placenta CDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (sites)
AUTHORS Tateishi,S., Sakuraba,Y., Masuyama,S., Inoue,H. and Yamazumi,M.
TITLE Dysfunction of human Rad18 results in defective postreplication
repair and hypersensitivity to multiple mutagens
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7927-7932 (2000)
MEDLINE 20345089
PUBMED
REFERENCE 2 (bases 1 to 2890)
AUTHORS Tateishi,S., Yamazumi,M. and Inoue,H.
TITLE Direct Submision
JOURNAL Submitted (26-NOV-1999) Satoshi Tateishi, Kumamoto University,
Institute of Molecular Embryology; Kuhnaji 4-24-1, Kumamoto,
Kumamoto 862-0976, Japan (E-mail:tateegpo.kumamoto-u.ac.jp),
Tel:81-096-373-6602, Fax:81-096-373-6604)
FEATURES
source Location/Qualifiers
1..2890
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/tissue_type="placenta"
1..2890
/gene="hRAD18"
126..1613
/gene="hRAD18"
/note="RING-zinc-finger protein"
/codon_start=1
/product="postreplication repair protein hRAD18p"
/protein_id="BA99284.1"
/db_xref="GI:8980617"
/translation="MDSLAEHRMPGLAVMKTIIDLLRCGICFEYFNIAITPPCSHN
YSCICIRKFLSYKTCPCVYTPEDDKNNRIIDELVYKSNAPRNHLQFALSPK
KEASPAKTKKRRVETIAPDPSEKRPPEPSTSLKQVTVDPVCGVNPESHINK
RHQEVHMINACCDLHPRKSAEIVQETENIEKTRMLKSLNESYVETFKDQTEKE
IDELHSKYRKRRKSEFQLVQARQYKRIAGMSQKVTYTKREESTKLSYCMQOE
DMWTSTYHNSQSLDSEPELEPDEEDSSCIDIOEVLSSSEDSNSSSDIIRDL
LEEEBAWEASHKNDLQDETISPQRRTFRAESAEIERKRNKN"
BASE COUNT 916 a 585 c 601 g 788 t
Query Match 46.0%; Score 69; DB 9; Length 2890;
Best Local Similarity 88.2%; Pred. No. 1.2e-11;
Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 51 GTGATCCCCCGGCTGCGAATTCGATATCAAGCTTATGATACCGTACCTCGAG 110
DB 2742 GTGATCCCCCGGCTGCGAATTCGATATCAAGCTTATGATACCGTACCTCGAG 2801
QY 111 GGGGCTACTACTAATTTGTT 135
DB 2802 GGGGCGCGGTACCACTTTGTT 2826
RESULT 15
AX247548
LOCUS
DEFINITION Sequence 1 from Patent WO0166775.
AX247548 2958 bp DNA linear PAT 28-SEP-2001

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:42:15 ; Search time 1350 Seconds

(without alignments)
1799.499 Million cell updates/sec

Title: US-08-935-377-9

Perfect score: 150

Sequence: 1 GGCCAAATGTGAAAACTA.....TTGTTTGTGGCGCCGCC 150

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estb:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_estc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_iny:*
20: em_gss_pln:*
21: em_gss_vtc:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75.4	50.3	891	14	B0140386
2	73.2	48.8	807	17	CNS06CT6
3	72.2	48.1	728	10	AM682547
4	72	48.0	182	13	B1306115
5	72	48.0	793	14	B0143916
6	70.4	46.9	841	17	CNS06M11

C	7	70	46.7	682	17	A0074693
C	8	69.8	46.5	361	17	CNS06CT6
C	9	69.8	46.5	804	14	B0158468
C	10	69.4	46.3	182	13	B1305962
C	11	69.4	46.3	186	13	B1305695
C	12	69.4	46.3	742	17	CNS06V04
C	13	69.2	46.1	912	17	CNS06UF5
C	14	69	46.0	162	10	BE428068
C	15	69	46.0	370	17	CNS06ME2
C	16	69	46.0	400	9	AU234451
C	17	69	46.0	390	9	AU278852
C	18	68.8	45.9	864	13	A0937400
C	19	68.8	45.9	175	13	B1306167
C	20	68.8	45.9	182	13	B1306149
C	21	68.8	45.9	182	13	B1306159
C	22	68.8	45.9	182	13	B1306178
C	23	68.8	45.9	182	13	B1306180
C	24	68.8	45.9	757	14	B0155148
C	25	68.4	45.6	152	17	CNS06TR4
C	26	68.2	45.5	312	13	BG919627
C	27	68	45.3	295	10	BE428455
C	28	68	45.3	608	17	A0009167
C	29	68	45.3	907	17	CNS06VTP
C	30	67.6	45.1	157	17	CNS06VER
C	31	67.6	45.1	829	17	A0937397
C	32	67.6	45.1	872	17	CNS06UB0
C	33	67.4	44.9	128	17	CNS07G34
C	34	67.4	44.9	528	17	B69688
C	35	67.4	44.9	801	17	CNS06WK6
C	36	67.4	44.9	902	17	CNS06WUM
C	37	67.2	44.8	240	17	CNS06VST
C	38	67	44.7	107	13	BM398556
C	39	67	44.7	108	17	BE492551
C	40	67	44.7	108	10	BE4292
C	41	67	44.7	124	10	AM914179
C	42	67	44.7	141	9	A0037147
C	43	67	44.7	141	17	B95279
C	44	67	44.7	144	17	B80294
C	45	67	44.7	157	12	BF281431

ALIGNMENTS

RESULT 1
LOCUS B0140386
DEFINITION NF035A10PH1081 Phoma-infected Medicago truncatula cDNA clone
ACCESSION NF035A10PH 5', mRNA sequence.
VERSION B0140386.1 GI:20276512
KEYWORDS EST.
SOURCE Medicago truncatula
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

REFERENCE 1 (bases 1 to 891)
AUTHORS Watson,B.S., Shin,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Inman,J.T., Waugh,M.E., Sullivan,J.P., May,G.D. and Paiva,N.L.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula Phoma-infected library
Unpublished (2002)
CONTACT: Paiva NL
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7317
Fax: 580 221 7380
Email: nlpaiva@noble.org
Insert length: 891 Std Error: 0.00

JOURNAL COMMENT

Plate: 035 row: A column: 10
Seq primer: TCACACGAGAAACGCTATGAC.
Location/Qualifiers
1. .891

FEATURES

SOURCE

/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF03A10PH"
/clone_1ib="Phoma-infected"
/tissue_type="leaf"
/dev_stage="pathogen-induced, young trifoliolate"
/note="Vector: phluescript SK(-): Young trifoliolate leaves of Medicago truncatula were excised and dip-inoculated in a spore suspension of Phoma medicaginis, and incubated in humid dishes. Pools of leaves were harvested at 0, 15, and 30 minutes and 1, 2, 3, 6, 14, 24, 48, 72, and 96, hours, and used to prepare total RNA. cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using Exasist helper phage and the E. coli strain XL1-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."

BASE COUNT 188 a 131 c 64 g 224 t 264 others
ORIGIN

Query Match

Best Local Similarity 87.8%; Score 75.4; DB 14; Length 891;
Pred. No. 1.3e-14;
Matches 79; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 51 GTGATCCCGGGCTGCAGAAATTCATATACCTTACCTCCAGCCGAGG 110
|||||
Db 84 GTGATCCCGGGCTGCAGAAATTCATATACCTTACCTCCAGCCGAGG 143
|||||
QY 111 GGGGGCTACTACTAATTTTCTTTTCT 140
|||||
Db 144 GGGGGCCGCGTANCTAATTTTNTCTATNT 173
|||||

RESULT 2
CNS06TYJ 807 bp DNA linear GSS 05-JUL-2001
LOCUS
DEFINITION T7 end of clone AX0AA003D05 of library AX0AA from strain CBS 7064
of Pichia farinosa, genomic survey sequence.
ACCESSION AL415169
VERSION AL415169.1 GI:12194040
KEYWORDS
SOURCE GSS.
ORGANISM Pichia farinosa.

REFERENCE

AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Lorente,B., Malpertuy,A., Neugejlise,C., Olier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies

TITLE

JOURNAL FEBS Lett. 487 (1), 3-12 (2000)

MEDLINE

20584711

PUBMED

11152876

AUTHORS

2 (bases 1 to 807)

TITLE

JOURNAL FEBS Lett. 487 (1), 87-90 (2000)

MEDLINE

20584725

PUBMED

REFERENCE

3 (bases 1 to 807)
Genoscope.
Direct Submission
Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 Evry cedex, FRANCE. (E-mail :
seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT

This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces marxianus var. marxianus, Pichia lactic var. lactic, Kluyveromyces Hansenii, Pichia sorbitophila, angusta, Debaryomyces Hansenii var. Hansenii, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

Location/Qualifiers
1. .807

/organism="Pichia farinosa"
/strain="CBS 7064"
/db_xref="taxon:4920"
/clone="AX0AA003D05"
/clone_1ib="AX0AA"
/note="end : T7"
BASE COUNT 230 a 186 c 125 g 218 t 48 others
ORIGIN

Query Match

Best Local Similarity 79.1%; Score 73.2; DB 17; Length 807;
Pred. No. 7.1e-14;
Matches 87; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 8 AATTGAAAACGTAGATCTATTATTGACCGCGCCGACATACGTGATCCCGGCTG 67
|||||
Db 243 AATTTCAGCAATTTGAGTTTTCATCGAAGAGATATTCAGCGATCCCGGCTG 302
|||||
QY 68 CAGGATTTGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCC 117
|||||
Db 303 CAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCC 352
|||||

RESULT 3
AM682547/C 728 bp mRNA linear EST 14-APR-2000
LOCUS
DEFINITION EST01410 E8.5 mouse craniofacial subtraction cDNA library Mus
musculus cDNA clone e064, mRNA sequence.
ACCESSION AM682547
VERSION AM682547.1 GI:7557255
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus.

REFERENCE

AUTHORS Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 728)
MuraKami,Y., Li,H., Chowdhury,S., Yamada,K.M. and Yamada,Y.
EST sequences from E8.5 mouse craniofacial cDNA library

JOURNAL

Unpublished (2000)

Contact: Yoshihiko Yamada

Craniofacial Developmental Biology and Regeneration Branch

National Institute of Dental and Craniofacial Research

9000 Rockville Pike, Building 30, Room 405, NIDCR, NIH, Bethesda,

MD 20892

Tel: 301 496 2111

Fax: 301 402 0897

Email: yoshi.yamada@nih.gov

Seq primer: M13 reverse.

Location/Qualifiers
1. .728

/organism="Mus musculus"
/strain="ICR"
/db_xref="taxon:10090"
/clone="e064"
/clone_1ib="E8.5 mouse craniofacial subtraction cDNA
library"

/tissue_type="craniofacial tissues"
/dev_stage="embryonic day 8.5"
/note="Vector: PT-Adv; A subtraction cDNA library was
constructed from E8.5 mouse craniofacial mRNA subextracted
from E13.5 mouse craniofacial mRNA."

BASE COUNT 191 a 158 c 179 g 188 t 12 others

ORIGIN

Query Match 48.1%; Score 72.2; DB 10; Length 728;
Best Local Similarity 78.9%; Pred. No. 1.5e-13;
Matches 86; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 37 GCGGCGCATGACGAGATCCCGGCTGAGGAATTCATATCACTTATGATAC 96
||||| |
Db 124 GCGGCGCTCGAGGGGATCCCGGCTGAGGAATTCATATCACTTATGATAC 65
||||| |

Qy 97 CGTGCACCTCGAGGGGCTTAACCTAATTTGTTTGTGGGCC 145
||||| |
Db 64 CGTGCACCTCGAGGGGCTTAACCTAATTTGTTTGTGGGCC 16
||||| |

RESULT 4
B1306115/c

LOCUS B1306115
DEFINITION B1306115 182 bp mRNA linear EST 20-JUL-2001
NL_3_G09 Drought stress (leaf) Oryza sativa cDNA clone NL_3_G09 3',
mRNA sequence.
ACCESSION B1306115
VERSION B1306115.1 GI:14981437
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 182)
Reddy,A.R., Ramakrishna,W., Chandrasekhar,A., Nagabushan,I.,
Rayindrababu,P. and Bennetzen,J.L.
Novel EST enrichment with normalized cDNA libraries from drought
stressed rice (Oryza sativa L.cv Nagina 22)
Unpublished (2001)
Contact: Reddy AR
Department of Plant Sciences, School of Life Sciences
University of Hyderabad
P.O. Central University, Hyderabad-500 046, A.P, India
Tel: 0091-40-3010265
Fax: 0091-40-3010145
Email: arjuls@uohyd.ernet.in
Insert Length: 182 Std Error: 0.00
Plate: 3 row: G column: 09
Seq primer: GTAAACGACGCGCCATG.
Location/Qualifiers
1..182
/organism="Oryza sativa"
/cultivar="Nagina 22 (Indica sub sp.)"
/db_xref="taxon:4530"
/clone="NL_3_G09"
/clone_lib="Drought stress (leaf)"
/tissue_type="Entire leaf tissue"
/dev_stage="35 day-old seedlings"
/note="Organ: Leaf; Vector: VTJ3pac; ESTs from normalized
leaf cDNA library from drought stressed seedlings"

BASE COUNT 34 a 47 c 53 g 48 t

ORIGIN

Query Match 48.0%; Score 72; DB 13; Length 182;
Best Local Similarity 93.8%; Pred. No. 1.7e-13;
Matches 75; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 51 GTGATCCCGGCTGAGGATTCATATCACTTATGATACCGTGCACCTGAGG 110
||||| |
Db 107 GTGATCCCGGCTGAGGATTCATATCACTTATGATACCGTGCACCTGAGG 48
||||| |

Qy 111 GGGGCGCTTAACCTAATTT 130

||||| |
Db 47 GCGGCGCGAGTACCACTT 28
||||| |

RESULT 5
B0143916

LOCUS B0143916
DEFINITION B0143916 793 bp mRNA linear EST 24-APR-2002
NF038H04DT1F1041 Drought Medicago truncatula cDNA clone NF038H04DT
5', mRNA sequence.
ACCESSION B0143916
VERSION B0143916.1 GI:20280975
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
1 (bases 1 to 793)
Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
truncatula drought library
Unpublished (2000)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 793 Std Error: 0.00
Plate: 038 row: H column: 04
Seq primer: TCACACGAGAAACGCTATGAC.
Location/Qualifiers
1..793
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF038H04DT"
/clone_lib="Drought"
/tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entire
plantlets harvested in a series of days-post-watering
timepoints."

BASE COUNT 217 a 203 c 205 g 168 t

ORIGIN

Query Match 48.0%; Score 72; DB 14; Length 793;
Best Local Similarity 93.8%; Pred. No. 1.8e-13;
Matches 75; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 51 GTGATCCCGGCTGAGGATTCATATCACTTATGATACCGTGCACCTGAGG 110
||||| |
Db 85 GTGATCCCGGCTGAGGATTCATATCACTTATGATACCGTGCACCTGAGG 144
||||| |

Qy 111 GGGGCGCTTAACCTAATTT 130
||||| |
Db 145 GGGGCGCGAGTACCACTT 164
||||| |

RESULT 6
CNS06W11

LOCUS CNS06W11 841 bp DNA linear GSS 06-JUL-2001
T7 end of clone AX0A027B04 of library AX0A from strain CBS 7064
of Pichia farinosa, genomic survey sequence.
ACCESSION AL417851
VERSION AL417851.1 GI:12200086
KEYWORDS GSS.
SOURCE Pichia farinosa.
ORGANISM Pichia farinosa
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.

REFERENCE 1 (bases 1 to 841)
AUTHORS Souciet,J., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neveuglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekai,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Winkler,P. and Weissbach,J.
TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
PUBMED 11152876
REFERENCE 2 (bases 1 to 841)
AUTHORS de Montigny,J., Spehner,C., Souciet,J., Tekai,F., Dujon,B.,
Winkler,P., Artiguenave,F. and Potier,S.
TITLE Genomic exploration of the hemiascomycetous yeasts: 15. *Pichia*
sorbitophila
JOURNAL FEBS Lett. 487 (1), 87-90 (2000)
MEDLINE 20584725
PUBMED 11152890
REFERENCE 3 (bases 1 to 841)
AUTHORS Direct Submission
TITLE Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
secref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This GSS is part of a random genomic sequencing program of thirteen
yeast species: *Saccharomyces bayanus* var. *varium*, *Saccharomyces*
exiguus, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*,
Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces*
lactis var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia*
angusta, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*,
Candida tropicalis and *Yarrowia lipolytica*. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
FEATURES
source
1. .841
/organism="Pichia farinosa"
/db_xref="taxon:4920"
/clone="AX0AA027B04"
/clone_1lb="AX0AA"
/note="end : T7"
BASE COUNT 238 a 174 c 246 g 182 t 1 others
ORIGIN
Query Match 46.9%; Score 70.4; DB 17; Length 841;
Best Local Similarity 98.6%; Pred. No. 6.2e-13;
Matches 71; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 46 ATGACGTGATCCCCGGGCTGACGAATTCGATATCACTTATCGATACCGTCGACT 105
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 744 ATGACGAGAGATCCCCGGGCTGCGAGATTGATATCACTTATCGATACCGTCGACT 803
QY 106 CGAGGGGGGGGCC 117
||||| |||||||
DB 804 CGAGGGGGGGGCC 815
RESULT 7
LOCUS A0074693/c 682 bp DNA linear GSS 20-AUG-1998
DEFINITION CIT-HSP-2301L23.TF CIT-HSP Homo sapiens genomic clone 2301L23, DNA
sequence.
ACCESSION A0074693
VERSION A0074693.1 GI:3436811
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 682)

AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.
TITLE Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
JOURNAL Unpublished (1998)
COMMENT Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@ligr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tbdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
FEATURES
source
1. .682
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2301L23"
/clone_1lb="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelBAC11; Site.1: HindIII; Site.2:
HindIII"
BASE COUNT 156 a 187 c 187 g 151 t 1 others
ORIGIN
Query Match 46.7%; Score 70; DB 17; Length 682;
Best Local Similarity 93.6%; Pred. No. 8.4e-13;
Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 51 GTGGATCCCCGGGCTGACGAATTCGATATCACTTATCGATACCGTCGAGG 110
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 78 GTGGATCCCCGGGCTGCGAGATTGATATCACTTATCGATACCGTCGAGG 19
QY 111 GGGGGCTTACTTACTAA 128
||||| |||||||
DB 18 GGGGGCGCCGAGTACCAG 1
RESULT 8
LOCUS CNS06CT6 361 bp DNA linear GSS 05-APR-2001
DEFINITION T7 end of clone AR0AA007H05 of library AR0AA from strain CBS 732 of
Zygosaccharomyces rouxii, genomic survey sequence.
ACCESSION AL392944.1 GI:12142764
VERSION AL392944.1
KEYWORDS GSS; clone AR0AA007H05; RST AR0AA007H05CPL.
SOURCE *Zygosaccharomyces rouxii*.
ORGANISM *Zygosaccharomyces rouxii*
REFERENCE Eukaryota; Fungi; Ascomycota; *Saccharomycotina*; *Saccharomycetes*;
Saccharomycetales; *Saccharomycetaceae*; *Zygosaccharomyces*.
1 (bases 1 to 361)
AUTHORS Souciet,J., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neveuglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekai,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Winkler,P. and Weissbach,J.
TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
PUBMED 11152876
REFERENCE 2 (bases 1 to 361)
AUTHORS de Montigny,J., Straub,M., Potier,S., Tekai,F., Dujon,B.,
Winkler,P., Artiguenave,F. and Souciet,J.
TITLE Genomic exploration of the hemiascomycetous yeasts: 8.
Zygosaccharomyces rouxii

/clone.lib="drought stress (leaf)"
 /tissue_type="Entire leaf tissue"
 /dev_stage="35 day-old seedlings"
 /note="Organ: Leaf; Vector: T7T3pac; ESTs from normalized
 leaf cDNA library from drought stressed seedlings"

BASE COUNT 34 a 48 c 52 g 46 t 2 others

Query Match 46.3%; Score 69.4; DB 13; Length 182;
 Best Local Similarity 91.2%; Pred. No. 1.3e-12;
 Matches 73; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 51 GTGATCCCGGGGCTGAGATTCGATTCAGCTTATCGATACCGTCGACCTGAGG 110
 |||||||
 DB 107 GTGATCCCGGGGCTGAGATTCGATTCAGCTTATCGATACCGTCGACCTGAGG 48

OY 111 GGGGGCCTAACTACTAATT 130
 |||||||
 DB 47 GGGGGCNCGGGTACCAATT 28

RESULT 11
 BI305695/c 186 bp mRNA linear EST 20-JUL-2001
 LOCUS NL_1.G23 drought stress (leaf) Oryza sativa cDNA clone NL_1.G23 3',
 DEFINITION mRNA sequence.
 ACCESSION BI305695
 VERSION BI305695.1 GI:14981017
 KEYWORDS EST.

SOURCE Oryza sativa.
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartioideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 186)
 Reddy,A.R., Kamakrishna,W., Chandrasekhar,A., Nagabhushan,I.,
 Ravindrababu,P. and Bennetzen,J.L.
 Novel EST enrichment with normalized cDNA libraries from drought
 stressed rice (Oryza sativa L.cv Nagina 22)
 JOURNAL Unpublished (2001)
 COMMENT Contact: Reddy AR
 Department of Plant Sciences, School of Life Sciences
 University of Hyderabad
 P.O. Central University, Hyderabad-500 046, A.P, India
 Tel: 0091-40-3010265
 Fax: 0091-40-3010145
 Email: arjulsleu@hyd.ernet.in
 Insert Length: 186 Std Error: 0.00
 Plate: 1 row: 6 column: 23
 Seq primer: GTAAACGAGCGCCAGTG.

FEATURES
 source
 1..186
 /organism="Oryza sativa"
 /cultivar="Nagina 22 (Indica sub sp)"
 /db_xref="taxon:4530"
 /clone="NL_1.G23"
 /clone.lib="Drought stress (leaf)"
 /tissue_type="Entire leaf tissue"
 /dev_stage="35 day-old seedlings"
 /note="Organ: Leaf; Vector: T7T3pac; ESTs from normalized
 leaf cDNA library from drought stressed seedlings"

BASE COUNT 35 a 47 c 56 g 46 t 2 others

Query Match 46.3%; Score 69.4; DB 13; Length 186;
 Best Local Similarity 91.2%; Pred. No. 1.3e-12;
 Matches 73; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 51 GTGATCCCGGGGCTGAGATTCGATTCAGCTTATCGATACCGTCGACCTGAGG 110
 |||||||
 DB 111 GTGATCCCGGGGCTGAGATTCGATTCAGCTTATCGATACCGTCGACCTGAGG 52
 OY 111 GGGGGCCTAACTACTAATT 130

DB 51 GGGGGCNCGGGTACCAATT 32
 |||||||

RESULT 12
 CNS06V04 742 bp DNA linear GSS 06-JUL-2001
 LOCUS T7 end of clone AX0A024B10 of library AX0A from strain CBS 7064
 DEFINITION of Pichia farinosa, genomic survey sequence.

ACCESSION AL417458
 VERSION AL417458.1 GI:12199166
 KEYWORDS GSS.

SOURCE Pichia farinosa.
 ORGANISM Pichia farinosa
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Saccharomycetaceae; Pichia.

REFERENCE 1 (bases 1 to 742)
 Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
 Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
 de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
 Malpertuy,A., Neugeglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
 Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
 Wincker,P. and Weissenbach,J.

Genomic exploration of the hemiascomycetous yeasts: 1. A set of
 yeast species for molecular evolution studies
 JOURNAL FEMS Lett. 487 (1), 3-12 (2000)
 MEDLINE 20584711
 PUBMED 11152876

REFERENCE 2 (bases 1 to 742)
 de Montigny,J., Spennet,C., Souciet,J., Tekala,F., Dujon,B.,
 Wincker,P., Artiguenave,F. and Potier,S.
 Genomic exploration of the hemiascomycetous yeasts: 15. Pichia
 sorbitophila

JOURNAL FEMS Lett. 487 (1), 87-90 (2000)
 MEDLINE 20584725
 PUBMED 11152890
 3 (bases 1 to 742)

REFERENCE Genoscope:
 Direct Submission
 Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
 seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 COMMENT This GSS is part of a random genomic sequencing program of thirteen
 yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
 exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
 Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
 lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
 angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
 Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
 5 kb were prepared and both extremities were sequenced. See
 keywords for description of this sequence and for the sequence of
 the other extremity of this insert.

FEATURES
 source
 1..742
 /organism="Pichia farinosa"
 /strain="CBS 7064"
 /db_xref="taxon:4920"
 /clone="AX0A024B10"
 /clone.lib="AX0A"
 /note="end : 77"
 /note="complement(<3..>641)
 /note="similar to Saccharomyces cerevisiae ORF YDR238c [

misc-feature
 SEC26 : coatomer complex beta chain of secretory pathway
 vesicles]"
 /evidence="not-experimental"

BASE COUNT 207 a 154 c 156 g 224 t 1 others

Query Match 46.3%; Score 69.4; DB 17; Length 742;
 Best Local Similarity 83.2%; Pred. No. 1.3e-12;
 Matches 79; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 23 TCTATTATTGACGCGCGCCGATGATGATCCCGGGCTGAGATTCGATTC 82


```

Db      614 TCAATTACCGGTGTTGTCACACTTGGGGCAGATCCCGGGCTGCAGGAATTCGATATC 673
Oy      83 AAGCTTATCGATACCGTCGACCTCGAGGGGGGGGCC 117
Db      674 AAGCTTATCGATACCGTCGACCTCGAGGGGGGGGCC 708

RESULT 13
CNS06UF5
LOCUS    912 bp    DNA    linear    GSS 06-JUL-2001
DEFINITION T7 end of clone AX0AA008E09 of library AX0A from strain CBS 7064
ACCESSION AL415767
VERSION   AL415767.1 GI:12195405
KEYWORDS  GSS.
SOURCE    Pichia farinosa.
ORGANISM  Pichia farinosa
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
REFERENCE 1 (bases 1 to 912)
AUTHORS   Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
deMontigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvéglise,C., Olier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
Yeast species for molecular evolution studies
JOURNAL   FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE   20584711
PUBMED    11152876
REFERENCE 2 (bases 1 to 912)
AUTHORS   de Montigny,J., Spehner,C., Souciet,J., Tekala,F., Dujon,B.,
Wincker,P., Artiguenave,F. and Potier,S.
Genomic exploration of the hemiascomycetous yeasts: 15. Pichia
sorbitophila
JOURNAL   FEBS Lett. 487 (1), 87-90 (2000)
MEDLINE   20584725
PUBMED    11152890
REFERENCE 3 (bases 1 to 912)
AUTHORS   Genoscope.
TITLE     Direct Submission
JOURNAL   Submitted (07-SEP-2000) Genoscope - Centre National de Séquençage,
2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces marxianus var. marxianus, Pichia
lactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
FEATURES
    source
        1..912
            /organism="Pichia farinosa"
            /strain="CBS 7064"
            /db_xref="taxon:4920"
            /clone="AX0AA008E09"
            /clone_1id="AX0AA"
            /note="end : T7"
BASE COUNT  298 a 210 c 160 g 240 t 4 others
ORIGIN
Query Match 46.1%; Score 69.2; DB 17; Length 912;
Best Local Similarity 88.1%; Pred. No. 1.6e-12;
Matches 74; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Oy      52 TGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 111
|||||

```

```

Db      817 TGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 876
Oy      112 GGGGCTACTACTACTAATTTTGT 135
Db      877 GGGGGCCCGGTACACAGCTTTTGT 900

RESULT 14
BE428068
LOCUS    162 bp    mRNA    linear    EST 26-JUL-2000
DEFINITION MDD002.H10F990615 ITFC MTD Durum wheat Root Library Triticum
turgidum subsp. durum cDNA clone MTD002.H10, mRNA sequence.
ACCESSION BE428068
VERSION   BE428068.1 GI:9425911
KEYWORDS  EST.
SOURCE    durum wheat.
ORGANISM  Triticum turgidum subsp. durum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 162)
AUTHORS   Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier
's., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P.,
Herrmann,R.G., Holtan,T., Jacquemart,J.M., Jia,J., Joudrier,P.,
Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y.,
Pechioni,N., Qawalser,C., Schuch,W., Selvaraj,G., Sharifou,M.,
Sorelli,M., Warburton,M. and Wenzel,G.
International Triticace EST Cooperative (ITEC): Production of
Expressed Sequence Tags for Species of the Triticeae
Unpublished (2000)
JOURNAL   INRA, Unite de Biochimie et Biologie Moléculaire des Cereales
COMMENT    Contact: Joudrier P
INRA, Unite de Biochimie et Biologie Moléculaire des Cereales
2, place VIALA, 34060 Montpellier cedex 01 FRANCE
Tel: 33 4 99 61 23 84
Fax: 33 4 99 61 23 48
Email: joudrier@enscm.inra.fr
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
FEATURES
    source
        1..162
            /organism="Triticum turgidum subsp. durum"
            /cultivar="Siliana"
            /db_xref="taxon:4567"
            /clone="MTD002.H10"
            /clone_1id="ITEC MTD Durum Wheat Root Library"
            /tissue_type="root"
            /dev_stage="3-day-old seedling, water-stressed"
            /note="Vector: pSPORT1, T7 primers used. See pSPORT1
polylinker site. 0.3-2.0 kbp average insert size."
BASE COUNT  28 a 42 c 49 g 43 t
ORIGIN
Query Match 46.0%; Score 69; DB 10; Length 162;
Best Local Similarity 88.2%; Pred. No. 1.7e-11;
Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy      51 GTGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
|||||
Db      24 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 83
Oy      111 GGGGGCTACTACTAATTTTGT 135
Db      84 GGGGGCCCGGTACACAGCTTTTGT 108

RESULT 15
CNS06WE2
LOCUS    370 bp    DNA    linear    GSS 06-JUL-2001
DEFINITION T7 end of clone AX0AA030G01 of library AX0A from strain CBS 7064
ACCESSION AL418320
VERSION   AL418320.1 GI:12200918
KEYWORDS  GSS.

```


GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 04:19:15 ; Search time 176.987 Seconds

(without alignments)
1908.619 Million cell updates/sec

Title: US-08-935-377-9

150

Perfect score: 1 GGCCTAAATTTGAAAACTA.....TTGTTTGTGTGGCCCGGCC 150

Sequence:

Scoring table: IDENTITY_NUC
Gap 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: N_Geneseq_101002.*
2: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
3: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
4: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
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6: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
7: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
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9: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
10: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
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19: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
20: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
21: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
25: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	150	100.0	150	21	AAA15238
2	150	100.0	150	22	ABA01479
3	150	100.0	150	24	AAD31781
4	138	92.0	149	21	AAA15237
5	138	92.0	149	22	ABA01478
6	138	92.0	149	24	AAD31780
7	136	90.7	148	21	AAA15236
8	136	90.7	148	22	ABA01477
9	136	90.7	148	24	AAD31779

10	130	86.7	145	21	AAA15235	Nucleotide sequenc
11	130	86.7	145	22	ABA01476	Partial p7.5/ATG3/
12	130	86.7	145	24	AAD31778	Modified p7.5/tk v
13	75	50.0	611	23	ABV42990	Human prostate exp
14	74.8	49.9	432	23	ABV38237	Human prostate exp
15	74.4	49.6	508	23	ABV39281	Human prostate exp
16	74.2	49.5	528	23	ABV38626	Human prostate exp
17	74	49.3	612	23	ABV34128	Human prostate exp
18	73.4	48.9	450	23	ABV38398	Human prostate exp
19	73.4	48.9	467	23	ABV45888	Human prostate exp
20	73.4	48.9	573	23	ABV38615	Human prostate exp
21	73	48.7	410	23	ABV38443	Human prostate exp
22	72.2	48.1	684	23	ABV36344	Human prostate exp
23	72.2	48.1	855	24	ABV45375	Human prostate exp
24	72.2	48.1	855	24	ABV60152	Human prostate exp
25	72	48.0	276	23	ABV35118	Fungi stress respo
26	71.8	47.9	372	23	ABV43508	Human prostate exp
27	71.8	47.9	393	23	ABV36203	Human prostate exp
28	71.8	47.9	393	23	ABV45252	Human prostate exp
29	71.8	47.9	408	23	ABV45252	Human prostate exp
30	71.8	47.9	416	23	ABV35567	Human prostate exp
31	71.8	47.9	417	23	ABV38388	Human prostate exp
32	71.8	47.9	465	23	ABV42673	Human prostate exp
33	71.8	47.9	466	23	ABV35226	Human prostate exp
34	71.8	47.9	469	23	ABV42812	Human prostate exp
35	71.8	47.9	474	23	ABV34198	Human prostate exp
36	71.8	47.9	474	23	ABV43059	Human prostate exp
37	71.8	47.9	565	23	ABV34124	Human prostate exp
38	71.8	47.9	565	23	ABV42886	Human prostate exp
39	71.8	47.9	615	23	ABV38816	Human prostate exp
40	71.8	47.9	619	23	ABV32153	Human prostate exp
41	71.6	47.7	460	23	ABV33323	Human prostate exp
42	71.6	47.7	460	23	ABV42246	Human prostate exp
43	71.4	47.6	410	23	ABV32098	Human prostate exp
44	71.4	47.6	410	23	ABV41036	Human prostate exp
45	71.4	47.6	426	23	ABV38236	Human prostate exp

ALIGNMENTS

RESULT 1	AAA15238	standard; DNA; 150 BP.
ID	AAA15238	
XX	AAA15238;	
AC	04-SEP-2000	(first entry)
DT		
XX		
DE		Nucleotide sequence of a fragment of the plasmid p7.5/ATG3/tk.
XX		
KW		Vaccinia transfer plasmid; epitope; tumour specific epitope; antigen.
KW		vaccine; tumour regression; cancer; infection; ss.
XX		
OS		Synthetic.
XX		
PN		WO200028016-A1.
PD		18-MAY-2000.
XX		
PF		10-NOV-1998; 98WO-US24029.
XX		
PR		10-NOV-1998; 98WO-US24029.
XX		
PA		(UTRP) UNITV ROCHESTER.
XX		
PI		Zauderer M;
XX		
DR		WPI; 2000-376533/32.
XX		
PT		Novel method of identifying target epitopes or antigens specific for
PT		human tumors, cancers and infected cells involving screening expression
PT		library products of a cell expressing the target epitope

PD 14-FEB-2002.
XX
XX 02-APR-2001; 2001US-0822250.
XX
XX 22-SEP-1997; 97US-0935377.
XX
XX (UVRP) UNIV ROCHESTER.
XX
XX Zauderer M;
XX
XX WPI: 2002-239252/29.
XX
XX
XX Representational difference Analysis method for identification of
XX antigens recognized by cytotoxic T cells and specific for human tumors,
XX comprises improved selection of genes encoding target antigens -
XX
XX Example 1; Fig 2; 54pp; English.
XX
XX The present invention relates to novel methods for the identification
XX of antigens recognised by cytotoxic T cells (CTIs) and specific for
XX human tumors, cancers and infected cells. The method involves screening
XX the products of an expression library generated from DNA/RNA of a cell
XX expressing a target epitope with cytotoxic T cells generated against
XX the cell to identify DNA clones expressing target epitope or providing
XX cytotoxic T cells specific for a gene product differentially expressed
XX for cells expressing a target epitope in which the target epitope is
XX identified as a gene product inducing cytotoxic T cells. The method is
XX useful for identifying a target epitope or antigen specific for a tumour
XX cell. The target epitope is also useful for identifying target for a tumour
XX in other target cells against which it is desirable to induce cell-
XX mediated immunity. The antigen identified by the method is useful
XX in immunogenic compositions and vaccine preparations to induce the
XX regression of tumors, cancers and infections in mammals. The invention
XX also relates to vaccinia viral vectors which are useful for treating
XX tumour-bearing mammals, including humans to generate immune response
XX against the tumour cells. They are also useful for immunising or
XX vaccinating tumour-free subjects to prevent tumour formation. The
XX present sequence is modified p7.5/tk (thymidine kinase) vector.
XX p7.5/ATG3/tk. This vector comprises a vaccinia virus 7.5K promoter and
XX a modified tk DNA fragment. This vector is used in the exemplification
XX of the invention.
XX
XX Sequence 150 BP; 36 A; 38 C; 39 G; 37 T; 0 other;
XX
XX Query Match 100.0%; Score 150; DB 24; Length 150;
XX Best Local Similarity 100.0%; Pred. No. 1e-42;
XX Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 0Y 1 GGGCAAAAATTGAAAACCTAGATCTATTATTGACGCGCGCCGATGAGTCCCC 60
XX |||||||
XX DB 1 GGGCAAAAATTGAAAACCTAGATCTATTATTGACGCGCGCCGATGAGTCCCC 60
XX
XX 0Y 61 CGGCGTGCAGGAATTCGATATCAAGCTTATGATACCGTGCAGCGGGGGGCTTAA 120
XX |||||||
XX DB 61 CGGCGTGCAGGAATTCGATATCAAGCTTATGATACCGTGCAGCGGGGGGCTTAA 120
XX
XX 0Y 121 CTAAGTAAATTTGTTTGTGGGCCCGGCC 150
XX |||||||
XX DB 121 CTAAGTAAATTTGTTTGTGGGCCCGGCC 150
XX
XX
XX RESULT 4
XX AAA15237
XX ID AAA15237 standard; DNA: 149 BP.
XX
XX AAA15237;
XX
XX 04-SEP-2000 (first entry)
XX
XX Nucleotide sequence of a fragment of the plasmid p7.5/ATG2/tk.
XX
XX Vaccinia transfer plasmid; epitope; tumour specific epitope; antigen;

KW vaccine; tumour regression; cancer; infection; ss.
XX
XX Synthetic.
XX
XX WO200028016-A1.
XX
XX 18-MAY-2000.
XX
XX 10-NOV-1998; 98WO-US24029.
XX
XX 10-NOV-1998; 98WO-US24029.
XX
XX 10-NOV-1998; 98WO-US24029.
XX
XX (UVRP) UNIV ROCHESTER.
XX
XX Zauderer M;
XX
XX WPI: 2000-376533/32.
XX
XX
XX Novel method of identifying target epitopes or antigens specific for
XX human tumors, cancers and infected cells involving screening expression
XX library products of a cell expressing the target epitope -
XX
XX Disclosure; Fig 2; 132pp; English.
XX
XX The present sequence represents a fragment of a vaccinia transfer
XX plasmid, which is used in the course of the invention. The
XX specification describes a method for identifying a target epitope.
XX The method comprises screening the products of an expression library
XX from a cell expressing the target epitope with cytotoxic T cells
XX generated against the cell to identify DNA clones expressing the target
XX epitope. The method may also comprise providing a cytotoxic T cell
XX specific for a gene product differentially expressed by a cell and
XX measuring the cross-reactivity of the cytotoxic T cell. The methods are
XX useful for identifying tumour specific target epitopes and antigens which
XX are useful in immunogenic compositions or vaccines to induce the
XX regression of tumors, cancers or infections in mammals. The genes
XX expressed in a panel of tumour cells that are derived from single
XX immortalised, non-tumorigenic cell line are used to generate HLA
XX restricted cytotoxic T cells which are evaluated for activity against
XX tumour cells. The method is useful to identify potential antigens
XX expressed not only by the pathogen but also by the host cells whose gene
XX expression is altered as a result of infection. The differential gene
XX expression strategies can be applied to identify immunogenic molecules
XX of cells infected with virus, fungus or mycobacterium.
XX
XX Sequence 149 BP; 36 A; 37 C; 39 G; 37 T; 0 other;
XX
XX Query Match 92.0%; Score 138; DB 21; Length 149;
XX Best Local Similarity 99.3%; Pred. No. 1.7e-38;
XX Matches 149; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
XX 0Y 1 GGGCAAAAATTGAAAACCTAGATCTATTATTGACGCGCGCCGATGAGTCCCC 60
XX |||||||
XX DB 1 GGGCAAAAATTGAAAACCTAGATCTATTATTGACGCGCGCCGATGAGTCCCC 59
XX
XX 0Y 61 CGGCGTGCAGGAATTCGATATCAAGCTTATGATACCGTGCAGCGGGGGGCTTAA 120
XX |||||||
XX DB 60 CGGCGTGCAGGAATTCGATATCAAGCTTATGATACCGTGCAGCGGGGGGCTTAA 119
XX
XX 0Y 121 CTAAGTAAATTTGTTTGTGGGCCCGGCC 150
XX |||||||
XX DB 120 CTAAGTAAATTTGTTTGTGGGCCCGGCC 149
XX
XX
XX RESULT 5
XX ABA01478
XX ID ABA01478 standard; DNA: 149 BP.
XX
XX ABA01478;
XX
XX 04-FEB-2002 (first entry)
XX
XX Partial p7.5/ATG2/tk sequence.

```

XX Cell death; toxic gene; tumour suppressor; ds.
KM Synthetic.
OS
XX WO200172995-A2.
XX
XX 04-OCT-2001.
XX
XX 28-MAR-2001; 2001WO-US09953.
XX
XX 28-MAR-2000; 2000US-0192586.
XX
XX 10-MAY-2000; 2000US-0203343.
XX
XX 23-JAN-2001; 2001US-0263226.
XX
XX 27-FEB-2001; 2001US-0271426.
XX
XX (UNRP ) UNIV ROCHESTER.
XX
XX Zauderer M, Smith ES;
XX
XX WPI; 2001-570897/64.
XX
XX Selecting target polynucleotides, particularly toxic genes, involves
XX introducing a library of insert polynucleotides into a host cell
XX population, where the target polynucleotide promotes cell death -
XX
XX Disclosure; Fig 8; 359pp; English.
XX
XX The present invention relates to a method for selecting a target
XX polynucleotide. The method comprises introducing into a host cell
XX population a library of insert polynucleotides, where expression of the
XX target polynucleotide directly or indirectly promotes host cell death.
XX The cells are cultured and the insert polynucleotides are collected from
XX the cells which die. The method is useful for selecting target
XX polynucleotides, particularly polynucleotides which alter cell phenotypes
XX of induce or inhibit cell death. The method can be used to isolate toxic
XX genes such as tumour suppressors. The present sequence was used to
XX illustrate the method of the the present invention.
XX
XX Sequence 149 BP; 36 A; 37 C; 39 G; 37 T; 0 other;
XX
XX
XX Query Match          92.0%; Score 138; DB 22; Length 149;
XX Best Local Similarity 99.3%; Pred. No. 1.7e-38;
XX Matches 149; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
XX QY 1 GGGCAAAAATTTGAAAACCTAGATCTATTATTTCGACGGCGCCCATGACGTGATCCCC 60
XX      |||||||
XX Db 1 GGGCAAAAATTTGAAAACCTAGATCTATTATTTCGACGGCGCCCATGA-GTGGATCCCC 59
XX
XX QY 61 CGGCTGACGAGATTCGATTCAGATTCAGTACCGTCGACCTCGAGGGGGGCGCTAA 120
XX      |||||||
XX Db 60 CGGCTGACGAGATTCGATTCAGATTCAGTACCGTCGACCTCGAGGGGGGCGCTAA 119
XX
XX QY 121 CTAACCTAATTTGTTTTGTGGGGCCGCC 150
XX      |||||||
XX Db 120 CTAACCTAATTTGTTTTGTGGGGCCGCC 149
XX
XX
XX RESULT 6
XX AAD31780
XX ID AAD31780 standard; DNA; 149 BP.
XX
XX AAD31780;
XX
XX 18-JUN-2002 (first entry)
XX
XX Modified p7.5/tk vector, p7.5/ATG2/tk.
XX
XX Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;
XX vaccine; immune response; cytosolic; p7.5/tk vector; thymidine kinase;
XX p7.5/ATG2/tk vector; ds.
XX
XX Vaccinia virus.
XX

```

```

OS Synthetic.
XX
XX Key Location/Qualifiers
XX Key 46..48
XX misc_signal /*tag= a
XX /*note="Translation start codon"
XX 117..119
XX misc_signal /*tag= b
XX /*note="Translation stop codon"
XX 121..123
XX misc_signal /*tag= c
XX /*note="Translation stop codon"
XX 125..127
XX misc_signal /*tag= d
XX /*note="Translation stop codon"
XX 133..139
XX misc_signal /*tag= e
XX /*note="Transcription stop signal"
XX
XX US2002018785-A1.
XX
XX 14-FEB-2002.
XX
XX 02-APR-2001; 2001US-0822250.
XX
XX 22-SEP-1997; 97US-0935377.
XX
XX (UNRP ) UNIV ROCHESTER.
XX
XX Zauderer M;
XX
XX WPI; 2002-239252/29.
XX
XX Representational Difference Analysis method for identification of
XX antigens recognized by cytotoxic T cells and specific for human tumors,
XX comprises improved selection of genes encoding target antigens
XX
XX Example 1; Fig 2; 54pp; English.
XX
XX The present invention relates to novel methods for the identification
XX of antigens recognised by cytotoxic T cells (CTLs) and specific for
XX human tumours, cancers and infected cells. The method involves screening
XX the products of an expression library generated from DNA/RNA of a cell
XX expressing a target epitope with cytotoxic T cells generated against
XX the cell to identify DNA clones expressing target epitope or providing
XX cytotoxic T cells specific for a gene product differentially expressed
XX by a cell and measuring the cross-reactivity of the cytotoxic T cells
XX for cells expressing a target epitope in which the target epitope is
XX identified as a gene product inducing cytotoxic T cells. The method is
XX useful for identifying a target epitope or antigen specific for a tumour
XX cell. The target epitope is also useful for identifying target antigens
XX against the tumour cells against which it is desirable to induce cell-
XX mediated immunity. The antigen identified by the method is useful
XX in immunogenic compositions and vaccine preparations to induce the
XX regression of tumours, cancers and infections in mammals. The invention
XX also relates to vaccinia viral vectors which are useful for treating
XX tumour-bearing mammals, including humans to generate immune response
XX against the tumour cells. They are also useful for immunising or
XX vaccinating tumour-free subjects to prevent tumour formation. The
XX present sequence is modified p7.5/tk (thymidine kinase) vector,
XX p7.5/ATG2/tk. This vector comprises a vaccinia virus 7.5k promoter and
XX a modified tk DNA fragment. This vector is used in the exemplification
XX of the invention.
XX
XX Sequence 149 BP; 36 A; 37 C; 39 G; 37 T; 0 other;
XX
XX
XX Query Match          92.0%; Score 138; DB 24; Length 149;
XX Best Local Similarity 99.3%; Pred. No. 1.7e-38;
XX Matches 149; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
XX QY 1 GGGCAAAAATTTGAAAACCTAGATCTATTATTTCGACGGCGCCCATGACGTGATCCCC 60
XX      |||||||
XX Db 1 GGGCAAAAATTTGAAAACCTAGATCTATTATTTCGACGGCGCCCATGA-GTGGATCCCC 59
XX

```

QY 61 CGGGCTCAGGAATTCGATATCAAGCTTATCGATTACCTCGACCTCGAGGGGGGCTTAA 120
|
Db 60 CGGGCTCAGGAATTCGATATCAAGCTTATCGATTACCTCGACCTCGAGGGGGGCTTAA 119
QY 121 CTAACTAATTTTGTGTTTGTGGCCCGGCC 150
|
Db 120 CTAACTAATTTTGTGTTTGTGGCCCGGCC 149

RESULT 7
AAAI5236

ID AAI5236 standard; DNA; 148 BP.

AC AAI5236;

DT 04-SEP-2000 (first entry)

DE Nucleotide sequence of a fragment of the plasmid p7.5/ATG1/tk.

KM Vaccinia transfer plasmid; epitope; tumour specific epitope; antigen;

XX vaccine; tumour regression; cancer; infection; ss.

OS Synthetic.

PN WO200028016-A1.

PD 18-MAY-2000.

PF 10-NOV-1998; 98WO-US24029.

PR 10-NOV-1998; 98WO-US24029.

PA (UYRP) UNIV ROCHESTER.

PI Zauderer M;

XX WPI: 2000-376533/32.

DR Novel method of identifying target epitopes or antigens specific for
XX human tumors, cancers and infected cells involving screening expression
XX library products of a cell expressing the target epitope
PS Disclosure: Fig 2; 132pp; English.

CC The present sequence represents a fragment of a vaccinia transfer
CC plasmid, which is used in the course of the invention. The
CC specification describes a method for identifying a target epitope.
CC The method comprises screening the products of an expression library
CC from a cell expressing the target epitope with cytotoxic T cells
CC generated against the cell to identify DNA clones expressing the target
CC epitope. The method may also comprise providing a cytotoxic T cell
CC specific for a gene product differentially expressed by a cell and
CC measuring the cross-reactivity of the cytotoxic T cell. The methods are
CC useful for identifying tumour specific target epitopes and antigens which
CC are useful in immunogenic compositions or vaccines to induce the
CC regression of tumors, cancers or infections in mammals. The genes
CC expressed in a panel of tumour cells that are derived from single
CC immortalised, non-tumorigenic cell line are used to generate HLA
CC restricted cytotoxic T cells which are evaluated for activity against
CC tumour cells. The method is useful to identify potential antigens
CC expressed not only by the pathogen but also by the host cells whose gene
CC expression is altered as a result of infection. The differential gene
CC expression strategies can be applied to identify immunogenic molecules
CC of cells infected with virus, fungus or mycobacterium.

XX Sequence 148 BP; 35 A; 37 C; 39 G; 37 T; 0 other;

QY Query Match 90.7%; Score 136; DB 21; Length 148;

Best Local Similarity 98.7%; Pred. No. 8.4e-38;

Matches 148; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
QY 1 GGCCAAAATTTGAAAACTAGATCTATTATTCACGCGCGCCCATGACGTGATCCCC 60

Db |
|
QY 61 CGGGCTCAGGAATTCGATATCAAGCTTATCGATTACCTCGACCTCGAGGGGGGCTTAA 120
|
Db 59 CGGGCTCAGGAATTCGATATCAAGCTTATCGATTACCTCGACCTCGAGGGGGGCTTAA 118
QY 121 CTAACTAATTTTGTGTTTGTGGCCCGGCC 150
|
Db 119 CTAACTAATTTTGTGTTTGTGGCCCGGCC 148

RESULT 8
ABA01477

ID ABA01477 standard; DNA; 148 BP.

AC ABA01477;

DT 04-FEB-2002 (first entry)

DE Partial p7.5/ATG1/tk sequence.

XX Cell death; toxic gene; tumour suppressor; ds.

OS Synthetic.

PN WO200172995-A2.

PD 04-OCT-2001.

PF 28-MAR-2001; 2001WO-US09953.

PR 28-MAR-2000; 2000US-0192586.

PA 10-MAY-2000; 2000US-0203343.

PR 23-JAN-2001; 2001US-0263226.

PR 27-FEB-2001; 2001US-0271426.

PA (UYRP) UNIV ROCHESTER.

PI Zauderer M, Smith ES;

XX WPI: 2001-570897/64.

DR Selecting target polynucleotides, particularly toxic genes, involves
XX introducing a library of insert polynucleotides into a host cell
XX population, where the target polynucleotide promotes cell death -
PS Disclosure: Fig 8; 359pp; English.

CC The present invention relates to a method for selecting a target
CC polynucleotide. The method comprises introducing into a host cell
CC population a library of insert polynucleotides, where expression of the
CC target polynucleotide directly or indirectly promotes host cell death.
CC The cells are cultured and the insert polynucleotides are collected from
CC the cells which die. The method is useful for selecting target
CC polynucleotides, particularly polynucleotides which alter cell phenotypes
CC of induce or inhibit cell death. The method can be used to isolate toxic
CC genes such as tumour suppressors. The present sequence was used to
XX illustrate the method of the the present invention.

XX Sequence 148 BP; 35 A; 37 C; 39 G; 37 T; 0 other;

QY Query Match 90.7%; Score 136; DB 22; Length 148;

Best Local Similarity 98.7%; Pred. No. 8.4e-38;

Matches 148; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
QY 1 GGCCAAAATTTGAAAACTAGATCTATTATTCACGCGCGCCCATGACGTGATCCCC 60

Db 1 GGCCAAAATTTGAAAACTAGATCTATTATTCACGCGCGCCCATG--GTGATCCCC 58

QY 61 CGGGCTCAGGAATTCGATATCAAGCTTATCGATTACCTCGACCTCGAGGGGGGCTTAA 120
|
Db 59 CGGGCTCAGGAATTCGATATCAAGCTTATCGATTACCTCGACCTCGAGGGGGGCTTAA 118

OY	121	CTACGTAATTGTGTTTGAGGCCCGGC	150
Db	119	CTACGTAATTGTGTTTGAGGCCCGGC	148
RESULT	9		
AAD31779	ID	AAD31779 standard; DNA; 148 BP.	
XX	AC		
XX	AA	D31779;	
XX	DT	18-JUN-2002 (first entry)	
XX	DE	Modified p7.5/Lk vector, p7.5/ATG1/Lk.	
XX	KW	Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;	
KM	RN	vaccine; immune response; cytostatic; p7.5/Lk vector; thymidine kinase;	
KW	RV	p7.5/ATG1/Lk vector; ds.	
XX	OS	Vaccinia virus.	
OS	XX	Synthetic.	
XX	Key	Location/Qualifiers	
FT	FT	46..48	
FT	FT	/tag= a	
FT	FT	/note= "translation start codon"	
FT	FT	116..118	
FT	FT	/tag= b	
FT	FT	/note= "translation stop codon"	
FT	FT	120..122	
FT	FT	/tag= c	
FT	FT	/note= "translation stop codon"	
FT	FT	124..126	
FT	FT	/tag= d	
FT	FT	/note= "translation stop codon"	
FT	FT	132..138	
FT	FT	/tag= e	
FT	FT	/note= "transcription stop signal"	
PN	XX		
US2002018785-A1.			
PD	XX		
14-FEB-2002.			
XX	PF	02-APR-2001; 2001US-0822250.	
XX	PR	22-SEP-1997; 97US-0935377.	
PA	XX	(UVRP) UNIV ROCHESTER.	
XX	PI	Zauderer M;	
XX	DR	WPI; 2002-239252/29.	
PT	XX	Representational Difference Analysis method for identification of	
PT	XX	antigens recognised by cytotoxic T cells and specific for human tumors,	
PT	XX	comprises improved selection of genes encoding target antigens -	
XX	XX		
XX	XX	Example 1; Fig 2; 5app; English.	
XX	XX	The present invention relates to novel methods for the identification	
CC	CC	of antigens recognised by cytotoxic T cells (CTLs) and specific for	
CC	CC	human tumours, cancers and infected cells. The method involves screening	
CC	CC	the products of an expression library generated from DNA/RNA of a cell	
CC	CC	expressing a target epitope with cytotoxic T cells generated against	
CC	CC	the cell to identify DNA clones expressing target epitope or providing	
CC	CC	cytotoxic T cells specific for a gene product differentially expressed	
CC	CC	by a cell and measuring the cross-reactivity of the cytotoxic T cells	
CC	CC	for cells expressing a target epitope in which the target epitope is	
CC	CC	identified as a gene product inducing cytotoxic T cells. The method is	
CC	CC	useful for identifying a target epitope or antigen specific for a tumour	
CC	CC	cell. The target epitope is also useful for identifying target antigens	
CC	CC	in other target cells against which it is desirable to induce cell-	

CC mediated immunity. The antigen identified by the method is useful
CC in immunogenic compositions and vaccine preparations to induce the
CC regression of tumours, cancers and infections in mammals. The invention
CC also relates to vaccinia viral vectors which are useful for treating
CC tumour-bearing mammals, including humans to generate immune response
CC against the tumour cells. They are also useful for immunising or
CC vaccinating tumour-free subjects to prevent tumour formation. The
CC present sequence is modified p7.5/tk (thymidine kinase) vector,
CC p7.5/ATG/tk. This vector complies a vaccinia virus 7.5k promoter and
CC a modified tk DNA fragment. This vector is used in the exemplification
CC of the invention.

XX
SQ Sequence 148 BP; 35 A; 37 C; 39 G; 37 T; 0 other;

Query Match	90.7%;	Score 136;	DB 24;	Length 148;
Best Local Similarity	98.7%;	Pred. No. 8,4e-38;		
Matches 148;	Conservative 0;	Mismatches 0;	Indels 2;	Gaps
Dy 1	GGCAAAATTTGAAAACTGATCTATTATTATTCGACGCGCGGCCCATGAGCTGATCCCC	60		
Db 1	GGCAAAATTTGAAAACTGATCTATTATTATTCGACGCGCGGCCCATGAGCTGATCCCC	58		
Dy 61	CGGGCTGAGCAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCCTAA	120		
Db 59	CGGGCTGAGCAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCCTAA	118		
Dy 121	CTAACTAATTTTGTTTTGGGGCGCGGGC	150		
Db 119	CTAACTAATTTTGTTTTGGGGCGCGGGC	148		

CC	RESULT 10
XX	AAAI5235
XX	ID AAAI5235 standard; DNA; 145 BP.
XX	AC AAAI5235;
XX	DT 04-SEP-2000 (first entry)
XX	DE Nucleotide sequence of a fragment of the plasmid p7.5/ATG0/tk.
XX	KW Vaccinia transfer plasmid; epitope; tumour specific epitope; antigen;
XX	KW vaccine; tumour regression; cancer; infection; ss.
XX	OS Synthetic.
XX	PN WO200028016-A1.
XX	PD 18-MAY-2000.
XX	PF 10-NOV-1998; 98WO-US24029.
XX	PR 10-NOV-1998; 98WO-US24029.
XX	PA (UYRP) UNITV ROCHESTER.
XX	PI Zauderer M;
XX	DR WPI; 2000-376533/32.
XX	PT Novel method of identifying target epitopes or antigens specific for
XX	PT human tumors, cancers and infected cells involving screening expression
XX	PT library products of a cell expressing the target epitope -
XX	XX Disclosure; Fig 2; 132pp; English.
XX	XX The present sequence represents a fragment of a vaccinia transfer
XX	XX plasmid, which is used in the course of the invention. The
XX	XX specification describes a method for identifying a target epitope.
XX	XX The method comprises screening the products of an expression library
XX	XX from a cell expressing the target epitope with cytotoxic T cells
XX	XX generated against the cell to identify DNA clones expressing the target
XX	XX epitope. The method may also comprise providing a cytotoxic T cell

PT antigens recognized by cytotoxic T cells and specific for human tumors,
PT comprises improved selection of genes encoding target antigens -
XX
XX
PS Example 1: Fig 2: 54pp; English.

CC The present invention relates to novel methods for the identification
CC of antigens recognised by cytotoxic T cells (CTLs) and specific for
CC human tumors, cancers and infected cells. The method involves screening
CC the products of an expression library generated from DNA/RNA of a cell
CC expressing a target epitope with cytotoxic T cells generated against
CC the cell to identify DNA clones expressing target epitope or providing
CC cytotoxic T cells specific for a gene product differentially expressed
CC by a cell and measuring the cross-reactivity of the cytotoxic T cells
CC for cells expressing a target epitope in which the target epitope is
CC identified as a gene product inducing cytotoxic T cells. The method is
CC useful for identifying a target epitope or antigen specific for a tumour
CC cell. The target epitope is also useful for identifying target antigens
CC in other target cells against which it is desirable to induce cell-
CC mediated immunity. The antigen identified by the method is useful
CC in immunogenic compositions and vaccine preparations to induce the
CC regression of tumours, cancers and infections in mammals. The invention
CC also relates to vaccinia viral vectors which are useful for treating
CC tumour-bearing mammals, including humans to generate immune response
CC against the tumour cells. They are also useful for immunising or
CC vaccinating tumour-free subjects to prevent tumour formation. The
CC present sequence is modified p7.5/tk (thymidine kinase) vector,
CC p7.5/ATG0/kk. This vector comprises a vaccinia virus 7.5K promoter and
CC a modified tk DNA fragment. This vector is used in the exemplification
CC of the invention.
XX

SQ Sequence 145 BP; 34 A; 37 C; 38 G; 36 T; 0 other;

Query Match 86.7%; Score 130; DB 24; Length 145;
Best Local Similarity 96.7%; Pred. No. 1.1e-35;

Matches 145; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

YY 1 GGGCAAAATTTGAAACCTAGATCTATTATTATGACGCGCGCCGATGAGCTGATCCCC 60
DB 1 GGGCAAAATTTGAAACCTAGATCTATTATTATGACGCGCGCCGATGAGCTGATCCCC 55
YY 61 CGGGCTGACGAGATTCGATTCAGCTTATCGATACCGTGCAGGCGGGGCTTAA 120
DB 56 CGGGCTGACGAGATTCGATTCAGCTTATCGATACCGTGCAGGCGGGGCTTAA 115
YY 121 CTAACTAATTTTGTGTTGGGCGCGCC 150
DB 116 CTAACTAATTTTGTGTTGGGCGCGCC 145

RESULT 13

ABV42990
ID ABV42990 standard; cDNA; 611 BP.

XX ABV42990;

XX 16-SEP-2002 (first entry)

DE Human prostate expression marker cDNA 42981.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

KW pharmacogenomic marker; gene; ss.

XX Homo sapiens.

XX WO200160860-A2.

XX 23-AUG-2001.

XX 20-FEB-2001; 2001WO-US05171.

XX 17-FEB-2000; 2000US-183319P.

XX 16-MAR-2000; 2000US-189862P.

XX 25-MAY-2000; 2000US-207454P.

PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX

PS Claim 1; Page 8587-8588; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX

SQ Sequence 611 BP; 155 A; 142 C; 161 G; 149 T; 4 other;

Query Match 50.0%; Score 75; DB 23; Length 611;
Best Local Similarity 71.1%; Pred. No. 3.1e-16;

Matches 96; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

YY 1 GGGCAAAATTTGAAACCTAGATCTATTATTATGACGCGCGCCGATGAGCTGATCCCC 60
DB 437 GNNNNAAAAAAGTACCTCGCGCTGAGACTGATGATCCCC 496
YY 61 CGGGCTGACGAGATTCGATTCAGCTTATCGATACCGTGCAGGCGGGGCTTAA 120
DB 497 CGGGCTGACGAGATTCGATTCAGCTTATCGATACCGTGCAGGCGGGGCTTAA 556
YY 121 CTAACTAATTTTGTGTT 135
DB 557 TACCCAGCTTTGTT 571

RESULT 14

ABV38237
ID ABV38237 standard; cDNA; 432 BP.

XX ABV38237;

XX 16-SEP-2002 (first entry)

DE Human prostate expression marker cDNA 38228.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

KW pharmacogenomic marker; gene; ss.

XX Homo sapiens.

XX WO200160860-A2.

XX 23-AUG-2001.

XX 20-FEB-2001; 2001WO-US05171.

XX 17-FEB-2000; 2000US-183319P.

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PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PI Schlegel R, Endege WO, Monahan JE;
DR WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer -
PS Claim 1; Page 7801; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for:
XX (a) assessing whether a patient is afflicted with prostate cancer;
XX (b) monitoring the progression of prostate cancer in a patient;
XX (c) assessing the efficacy of a test compound to inhibit prostate
XX cancer in a patient;
XX (d) assessing the efficacy of a therapy for inhibiting prostate cancer
XX in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound;
XX (g) determining whether prostate cancer has metastasized in a patient;
XX (h) assessing the aggressiveness or indolence of prostate cancer in a
XX patient;
XX (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
SQ Sequence 432 BP; 118 A; 103 C; 105 G; 106 T; 0 other:
Query Match 49.9%; Score 74.8; DB 23; Length 432;
Best Local Similarity 72.4%; Pred. No. 3.2e-16;
Matches 97; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
QY 2 GCCAAAATTTGAAAACAGATCTATTATGACGCGCGCCGCCATGACGTGATCCGCC 61
DB 172 GCAAAATGTTTAAATTAACAAATTGACCTCGCGCTCTAGAACTAGTGATCCGCC 231
QY 62 GGGCTGCAGGAATTCGATCAAGCTTATCGATACCGTGCAGCTCGAGGGGGGCGCTAAC 121
DB 232 GGGCTGCAGGAATTCGATCAAGCTTATCGATACCGTGCAGCTCGAGGGGGGCGCGT 291
QY 122 TAACTAATTTGTT 135
DB 292 ACCCAGCTTTGTT 305
DB 292 ACCCAGCTTTGTT 305
RESULT 15
ABV39281
ID ABV39281 standard; cDNA; 508 BP.
XX
XX ABV39281;
AC
XX
XX 16-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 39272.
XX
XX Human prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX Homo sapiens.
XX
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US05171.

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XX
XX 17-FEB-2000; 2000US-183319P.
XX 16-MAR-2000; 2000US-189862P.
XX 25-MAY-2000; 2000US-207454P.
XX 09-JUN-2000; 2000US-211314P.
XX 18-JUL-2000; 2000US-219007P.
XX 13-DEC-2000; 2000US-255281P.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PI Schlegel R, Endege WO, Monahan JE;
DR WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer -
PS Claim 1; Page 7972; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for:
XX (a) assessing whether a patient is afflicted with prostate cancer;
XX (b) monitoring the progression of prostate cancer in a patient;
XX (c) assessing the efficacy of a test compound to inhibit prostate
XX cancer in a patient;
XX (d) assessing the efficacy of a therapy for inhibiting prostate cancer
XX in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound;
XX (g) determining whether prostate cancer has metastasized in a patient;
XX (h) assessing the aggressiveness or indolence of prostate cancer in a
XX patient;
XX (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
SQ Sequence 508 BP; 140 A; 115 C; 125 G; 128 T; 0 other:
Query Match 49.6%; Score 74.4; DB 23; Length 508;
Best Local Similarity 72.7%; Pred. No. 4.7e-16;
Matches 96; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY 4 CAAAATTTGAAAACAGATCTATTATGACGCGCGCCGCCATGACGTGATCCGCCG 63
DB 173 CAAAAGGACGTTTAAATTTGTACCTGCGCGCGCGCTGCAAGTGTGATCCGCCG 232
QY 64 GCTGCAGGAATTCGATCAAGCTTATCGATACCGTGCAGCTCGAGGGGGGCGCTACTA 123
DB 233 GCTGCAGGAATTCGATCAAGCTTATCGATACCGTGCAGCTCGAGGGGGGCGCGTAC 292
QY 124 ACTAATTTGTT 135
DB 293 CCAGCTTTTGT 304

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Search completed: November 10, 2002, 05:58:29
Job time: 177.987 secs

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OM nucleic - nucleic search, using sw model

Run on:

November 10, 2002, 05:58:40 ; Search time 37.3313 Seconds
(without alignments)
1425.554 Million cell updates/sec

Title: US-08-935-377-9

Perfect score: 150

Sequence: 1 GGGCAAAATTTGAAAACTA.....TTGTTTGTGTGGCCGGCC 150

Scoring table: IDENTITY_NUC

Gap 10.0 , Gapext 1.0

Searched: 320260 seqs, 177392727 residues

Total number of hits satisfying chosen parameters: 640520

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	150	100.0	150	10	US-09-822-250-9
2	150	100.0	150	10	US-09-987-456-5
3	138	92.0	149	10	US-09-822-250-8
4	138	92.0	149	10	US-09-987-456-4
5	136	90.7	148	10	US-09-822-250-7
6	136	90.7	148	10	US-09-987-456-3
7	130	86.7	145	10	US-09-822-250-6
8	130	86.7	145	10	US-09-987-456-2
9	69	46.0	424	10	US-09-834-975-601
10	67	44.7	118	10	US-09-784-130-9
11	67	44.7	457	10	US-09-735-705-306
12	67	44.7	457	10	US-09-850-716A-306
13	67	44.7	457	10	US-09-897-778-306
14	67	44.7	752	10	US-09-956-004-108
15	67	44.7	858	10	US-09-735-705-91
16	67	44.7	858	10	US-09-850-716A-91
17	67	44.7	858	10	US-09-897-778-91
18	66.8	44.5	545	10	US-09-810-935-10
19	66.8	44.5	545	10	US-09-429-755-10

C 20	65.8	43.9	574	10	US-09-834-975-541
C 21	64	42.7	661	10	US-09-912-447-16
C 22	62	41.3	105	10	US-09-974-300-7717
C 23	60	40.0	62	10	US-09-557-423-1
C 24	54.8	36.5	624	10	US-09-834-975-469
C 25	54.4	36.3	1094	10	US-09-932-418-3
C 26	51.2	34.1	4633	10	US-09-880-107-3822
C 27	50.4	33.6	332	10	US-09-823-114-14
C 28	49.8	33.2	1981	10	US-09-908-322-26
C 29	49.8	33.2	6244	10	US-09-281-674-8
C 30	49.8	33.2	6244	10	US-09-892-227-8
C 31	49.4	32.9	343	10	US-09-924-035A-839
C 32	49	32.7	1320	10	US-09-925-299-240
C 33	49	32.7	2790	10	US-09-739-254-30
C 34	48	32.0	53	10	US-09-904-615-30
C 35	48	32.0	57	10	US-09-822-250-23
C 36	48	32.0	57	10	US-09-955-649-4
C 37	48	32.0	57	10	US-09-973-013-4
C 38	48	32.0	57	10	US-09-987-456-1
C 39	48	32.0	57	10	US-09-822-250-1
C 40	48	32.0	69	10	US-09-987-456-1
C 41	48	32.0	69	10	US-09-822-250-1
C 42	48	32.0	100	10	US-09-987-456-140
C 43	47.8	31.9	362	10	US-09-380-728A-19
C 44	47	31.3	100	10	US-09-925-300-903
C 45	47	31.3	341	10	US-09-924-035A-737

Sequence 541, App
Sequence 16, Appl
Sequence 7717, Ap
Sequence 1, Appl1
Sequence 469, App
Sequence 3822, Ap
Sequence 26, Appl
Sequence 8, Appl1
Sequence 839, App
Sequence 240, App
Sequence 30, Appl
Sequence 23, Appl
Sequence 5, Appl1
Sequence 4, Appl1
Sequence 1, Appl1
Sequence 140, App
Sequence 19, Appl
Sequence 983, App
Sequence 737, App
Sequence 302, App

ALIGNMENTS

RESULT 1
US-09-822-250-9
Sequence 9, Application US/09822250
Patent No. US20020018785A1
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
FILE REFERENCE: 1821.0010001
CURRENT APPLICATION NUMBER: US/09/822,250
PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: US 08/935,377
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 150
TYPE: DNA
ORGANISM: synthetic construct
US-09-822-250-9

Query Match Best Local Similarity 100.0%; Score 150; DB 10; Length 150;
Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCAAAATTTGAAAACTAGATCTATTATTATTCACGCGCGGCATGACGTGATCCCC 60
DB 1 GGGCAAAATTTGAAAACTAGATCTATTATTATTCACGCGCGGCATGACGTGATCCCC 60
QY 61 GGGGCTGACGAGATTCGATTCACGCTTATCGATACCGTCGACCTCGAGGGGGCCCTAA 120
DB 61 GGGGCTGACGAGATTCGATTCACGCTTATCGATACCGTCGACCTCGAGGGGGCCCTAA 120
QY 121 CTAATAATTTGTTTGTGGCCCGGCC 150
DB 121 CTAATAATTTGTTTGTGGCCCGGCC 150

RESULT 2
US-09-987-456-5
Sequence 5, Application US/09987456
Patent No. US20020123057A1
GENERAL INFORMATION:

```
; APPLICANT: University of Rochester
; APPLICANT: Zauderer, Maurice
; APPLICANT: Ernest S. Smith
; TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
; TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells
; FILE REFERENCE: 1821.0070004
; CURRENT APPLICATION NUMBER: US/09/987,456
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/271,424
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/262,067
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/298,087
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/249,268
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 150
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p7.5/ATG3/lk vector
US-09-987-456-5

Query Match
Best Local Similarity 100.0%; Score 150; DB 10; Length 150;
Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 GGGCAAAAATGAAAACAGATCTATTATTGACAGCGCGCGCCGACGATGATCCG 60
    |||||||
DB 1 GGGCAAAAATGAAAACAGATCTATTATTGACAGCGCGCGCCGATGATGATCCG 60

QY 61 CGGGCTGCAGAGATTGCATATCAAGCTTACCGTCGACCTCGAGGGGGGCGCTAA 120
    |||||||
DB 61 CGGGCTGCAGAGATTGCATATCAAGCTTACCGTCGACCTCGAGGGGGGCGCTAA 120

QY 121 CTAACATAATTTGTTTGTGGGCCCGGCC 150
    |||||||
DB 121 CTAACATAATTTGTTTGTGGGCCCGGCC 150

RESULT 3
US-09-822-250-8
; Sequence 8, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
; CURRENT APPLICATION NUMBER: US/09/822,250
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 149
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-822-250-8
```

```
Query Match
Best Local Similarity 99.3%; Score 138; DB 10; Length 149;
Matches 149; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGGCAAAAATGAAAACAGATCTATTATTGACAGCGCGCGCCGATGATGATCCG 60
    |||||||
DB 1 GGGCAAAAATGAAAACAGATCTATTATTGACAGCGCGCGCCGATGATGATCCG 59

QY 61 CGGGCTGCAGAGATTGCATATCAAGCTTACCGTCGACCTCGAGGGGGGCGCTAA 120
    |||||||
```

```
DB 60 CGGGCTGCAGAGATTGCATATCAAGCTTACCGTCGACCTCGAGGGGGGCGCTAA 119
QY 121 CTAACATAATTTGTTTGTGGGCCCGGCC 150
    |||||||
DB 120 CTAACATAATTTGTTTGTGGGCCCGGCC 149
```

```
RESULT 4
US-09-987-456-4
; Sequence 4, Application US/09987456
; Patent No. US20020123057A1
; GENERAL INFORMATION:
; APPLICANT: University of Rochester
; APPLICANT: Zauderer, Maurice
; APPLICANT: Ernest S. Smith
; TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
; TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells
; FILE REFERENCE: 1821.0070004
; CURRENT APPLICATION NUMBER: US/09/987,456
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/271,424
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/262,067
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/298,087
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/249,268
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 149
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p7.5/ATG2/lk vector
US-09-987-456-4
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Query Match
Best Local Similarity 99.3%; Score 138; DB 10; Length 149;
Matches 149; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGGCAAAAATGAAAACAGATCTATTATTGACAGCGCGCGCCGACGATGATCCG 60
    |||||||
DB 1 GGGCAAAAATGAAAACAGATCTATTATTGACAGCGCGCGCCGATGATGATCCG 59

QY 61 CGGGCTGCAGAGATTGCATATCAAGCTTACCGTCGACCTCGAGGGGGGCGCTAA 120
    |||||||
DB 61 CGGGCTGCAGAGATTGCATATCAAGCTTACCGTCGACCTCGAGGGGGGCGCTAA 119

QY 121 CTAACATAATTTGTTTGTGGGCCCGGCC 150
    |||||||
DB 120 CTAACATAATTTGTTTGTGGGCCCGGCC 149
```

```
RESULT 5
US-09-822-250-7
; Sequence 7, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
; CURRENT APPLICATION NUMBER: US/09/822,250
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 148
; TYPE: DNA
; ORGANISM: synthetic construct
```

US-09-822-254-7

Query Match	90.7%;	Score 136;	DB 10;	Length 148;
Best Local Similarity	98.7%;	Pred. No. 4e-42;		
Matches 148;	Conservative	0;	Mismatches	0;
			Indels	2;
			Gaps	1

QY	1	GGCCAAAATTTGAAAACCTACATCTATTTTATTTGACGGGGGGCCATGACGTGGATGCC	60
QY	1	GGCCAAAATTTGAAAACCTACATCTATTTTATTTGACGGGGGGCCATGACGTGGATGCC <td>60</td>	60
Db	1	GGCCAAAATTTGAAAACCTACATCTATTTTATTTGACGGGGGGCCATGACGTGGATGCC	58
QY	61	CGGGGCTGAGGAATTCATATCAAGCCTTATGATACCGCTGACCTCGAGGGGGGGCCTAA	120
Db	59	CGGGGCTGAGGAATTCATATCAAGCCTTATGATACCGCTGACCTCGAGGGGGGGCCTAA	118
QY	121	CTAACAATATTTGTTTTGTGGGGCCGGCC	150
Db	119	CTAACAATATTTGTTTTGTGGGGCCGGCC	148

RESULT 6
US-09-987-456-3

```

GENERAL INFORMATION:
APPLICANT: University of Rochester
APPLICANT: Zauderer, Maurice
APPLICANT: Ernest S. Smith
TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells
FILE REFERENCE: 1821.0070004
CURRENT APPLICATION NUMBER: US/09/987,456
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/271,424
PRIOR FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 60/262,067
PRIOR FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: 60/298,087
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/249,268
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 148
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: p 7.5/ATG1/tk promoter
IS-09-987-456-3

```

Query Match	90.7%;	Score 136;	DB 10;	Length 148;
Best Local Similarity	98.7%;	Pred. No. 4e-42;		
Matches 148; Conservative	0;	Mismatches	0;	Indels 2; Gaps 1;

[illegible]

RESULT 7
US-09-822-250-6
; Sequence 6, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice

```

? TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
? FILE REFERENCE: 1821.0010001
? CURRENT APPLICATION NUMBER: US/09/822,250
? CURRENT FILING DATE: 2001-04-02
? PRIOR APPLICATION NUMBER: US 08/935,377
? PRIOR FILING DATE: 1997-09-22
? NUMBER OF SEQ ID NOS: 37
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO: 6
? LENGTH: 145
? TYPE: DNA
? ORGANISM: synthetic construct
US-09-822-250-6

Query Match      86.7%;   Score 130;   DB 10;   Length 145;
Best Local Similarity 96.7%;   Pred. No. 7,4e-40;
Matches 145; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

```

Query Match	86.7%;	Score 130;	DB 10;	Length 145;
Best Local Similarity	96.7%;	Pred. No. 7.4e-40;		
Matches 145;	Conservative	0;	Mismatches 0;	Indels 5; Gaps 1;

Oy	1	GGCCCAAAATTTGAAAAAATAGATCTATATTTATTTGACGCGGGCCGCGATCAGCTGGATGCC	60
	1	GGCCCAAAATTTGAAAAAATAGATCTATATTTATTTGACGCGGGCCGCGATCAGCTGGATGCC	60
Db	1	GGCCCAAAATTTGAAAAAATAGATCTATATTTATTTGACGCGGGCCGCGATCAGCTGGATGCC	55
Oy	61	CGGGGTGAGGAATTCGATATCAAGCTTATGATACGTCGACCTCGAGGGGGGGCCTAA	120
Db	56	CGGGGTGAGGAATTCGATATCAAGCTTATGATACGTCGACCTCGAGGGGGGGCCTAA	115
Oy	121	CTAACTAATTTTGTTTTGTGGGCCCGGCC	150
Db	116	CTAACTAATTTTGTTTTGTGGGCCCGGCC	145

```

RESULT 8
US-09-987-456-2
; Sequence 2, Application US/09987456
; Patent No. US20020123057A1
; GENERAL INFORMATION:
; APPLICANT: University of Rochester
; APPLICANT: Zauderer, Maurice
; APPLICANT: Ernest S. Smith
; TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
; TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells
; FILE REFERENCE: 1821.0070004
; CURRENT APPLICATION NUMBER: US/09/987,456
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/271,424
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/262,067
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/298,087
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/249,268
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 145
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p 7.5/ATG0/rk promoter
;S-09-987-456-2

```

Query Match	86.7%;	Score 130;	DB 10;	Length 145;
Best Local Similarity	96.7%;	Pred. No. 7.4e-40;		
Matches 145;	Conservative 0;	Mismatches 0;	Indels 5;	Gaps 1;

QY	1	GGGCAAAATTTGAAAACTAGATCTATTATTGACAGCGGCGCCCATGACGTGGATCCCC	60
Db	1	GGGCAAAATTTGAAAACTAGATCTATTATTTCACGCGAGCGCGC-----CGTGGATTCGCC	55
QY	61	CGGGCTGCAGGATTCGATTCATCAAGCTTATCGATTACCGTCGACCTCGAGGGGGGGGCTTAA	120
Db	56	CGGGCTGCAGGATTCGATTCATCAAGCTTATCGATTACCGTCGACCTCGAGGGGGGGGCTTAA	115

US-09-850-778A-306

Query Match
Best Local Similarity 44.7%; Score 67; DB 10; Length 457;
100.0%; Pred. No. 8.4e-16;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GTGATCCCCCGGGCTGCAGGATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
|||||
DB 360 GTGATCCCCCGGGCTGCAGGATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 419
QY 111 GGGGGCC 117
|||||
DB 420 GGGGGCC 426

RESULT 13

US-09-897-778-306
Sequence 306, Application US/09897778
Patent No. US20020147143A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Mannerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 306
LENGTH: 457
TYPE: DNA
ORGANISM: Homo sapiens
US-09-897-778-306

Query Match
Best Local Similarity 44.7%; Score 67; DB 10; Length 457;
100.0%; Pred. No. 8.4e-16;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GTGATCCCCCGGGCTGCAGGATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
|||||
DB 360 GTGATCCCCCGGGCTGCAGGATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 419
QY 111 GGGGGCC 117
|||||
DB 420 GGGGGCC 426

RESULT 14

US-09-956-004-108/C
Sequence 108, Application US/09956004
Patent No. US2002072595A1
GENERAL INFORMATION:
APPLICANT: Patrick J. Dillon et al.
TITLE OF INVENTION: Nucleotide Sequences of Escherichia coli Pathogenicity Islands
FILE REFERENCE: PB324D1
CURRENT APPLICATION NUMBER: US/09/956,004
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: 08/976,259
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/061,953
PRIOR FILING DATE: 1997-10-14
PRIOR APPLICATION NUMBER: 60/031,626
PRIOR FILING DATE: 1996-11-22
NUMBER OF SEQ ID NOS: 142
SOFTWARE: PatentIn version 3.1

SEQ ID NO 108
LENGTH: 752
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: misc_feature
LOCATION: (714)..(714)
OTHER INFORMATION: n equals a, t, g, or c
NAME/KEY: misc_feature
LOCATION: (719)..(719)
OTHER INFORMATION: n equals a, t, g, or c
US-09-956-004-108

Query Match
Best Local Similarity 44.7%; Score 67; DB 10; Length 752;
100.0%; Pred. No. 1.1e-15;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GTGATCCCCCGGGCTGCAGGATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
|||||
DB 72 GTGATCCCCCGGGCTGCAGGATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 13
QY 111 GGGGGCC 117
|||||
DB 12 GGGGGCC 6

RESULT 15

US-09-735-705-91
Sequence 91, Application US/09735705
Patent No. US2002052329A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 91
LENGTH: 858
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(858)
OTHER INFORMATION: n = A,T,C or G
US-09-735-705-91

Query Match
Best Local Similarity 44.7%; Score 67; DB 10; Length 858;
100.0%; Pred. No. 1.1e-15;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GTGATCCCCCGGGCTGCAGGATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
|||||
DB 357 GTGATCCCCCGGGCTGCAGGATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 416
QY 111 GGGGGCC 117
|||||
DB 417 GGGGGCC 423

Tue Nov 12 06:25:51 2002

Search completed: November 10, 2002, 11:33:47
job time : 38.3313 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:43:30 ; Search time 38.4558 Seconds

(Without alignments)
1196.219 Million cell updates/sec

Title: US-08-935-377-9

Sequence: 1 GCGCCAAATATGAAAACTA.....TTGTTTGTGCGCCGCCGCC 150

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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4: /cgn2_6/ptodata/1/1na/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/1na/PCtUS.COMB.seq:*
6: /cgn2_6/ptodata/1/1na/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69.8	46.5	793	US-08-967-101-121	Sequence 121, App
2	69.8	46.5	793	US-08-592-541-121	Sequence 121, App
3	69.8	46.5	793	US-09-124-698-121	Sequence 121, App
4	69.8	46.5	793	US-09-127-480-121	Sequence 121, App
5	69.8	46.5	793	US-08-496-841C-121	Sequence 121, App
6	69.8	46.5	793	US-09-124-523-121	Sequence 121, App
7	69.8	46.5	793	US-09-116-492A-39	Sequence 121, App
8	69.8	46.5	793	US-09-323-872A-26	Sequence 121, App
9	69.8	46.5	793	US-09-123-912-91	Sequence 121, App
10	69.8	46.5	793	US-09-123-912-91	Sequence 121, App
11	69.8	46.5	793	US-09-123-912-91	Sequence 121, App
12	69.8	46.5	793	US-09-123-912-91	Sequence 121, App
13	69.8	46.5	793	US-09-123-912-91	Sequence 121, App
14	69.8	46.5	793	US-09-123-912-91	Sequence 121, App
15	69.8	46.5	793	US-09-123-912-91	Sequence 121, App
16	69.8	46.5	793	US-09-123-912-91	Sequence 121, App
17	69.8	46.5	793	US-09-123-912-91	Sequence 121, App
18	69.8	46.5	793	US-09-123-912-91	Sequence 121, App
19	69.8	46.5	793	US-09-123-912-91	Sequence 121, App
20	69.8	46.5	793	US-09-123-912-91	Sequence 121, App
21	69.8	46.5	793	US-09-123-912-91	Sequence 121, App
22	69.8	46.5	793	US-09-123-912-91	Sequence 121, App
23	69.8	46.5	793	US-09-123-912-91	Sequence 121, App
24	69.8	46.5	793	US-09-123-912-91	Sequence 121, App
25	69.8	46.5	793	US-09-123-912-91	Sequence 121, App
26	69.8	46.5	793	US-09-123-912-91	Sequence 121, App
27	69.8	46.5	793	US-09-123-912-91	Sequence 121, App

28	65.4	43.6	5356	US-08-446-935-1	Sequence 1, Appl
29	65	43.3	78	US-09-462-645C-25	Sequence 25, Appl
30	65	43.3	84	US-09-462-645C-26	Sequence 26, Appl
31	65	43.3	698	US-08-998-416-54	Sequence 54, Appl
32	65	43.3	3465	US-09-462-645C-9	Sequence 9, Appl
33	65	43.3	3481	US-09-462-645C-11	Sequence 11, Appl
34	65	43.3	3794	US-09-462-645C-5	Sequence 5, Appl
35	65	43.3	3810	US-09-462-645C-7	Sequence 7, Appl
36	64.4	42.9	713	US-08-998-416-135	Sequence 135, Appl
37	62.4	41.6	685	US-08-463-115-56	Sequence 56, Appl
38	62.4	41.6	685	US-08-463-115-56	Sequence 56, Appl
39	59	39.3	4164	US-08-204-675-1	Sequence 1, Appl
40	59	39.3	4164	US-08-660-754-1	Sequence 1, Appl
41	59	39.3	4164	US-08-796-364-1	Sequence 1, Appl
42	59	39.3	4164	PCT-US95-02520-1	Sequence 1, Appl
43	58	38.7	5178	US-08-474-169-2	Sequence 2, Appl
44	57.8	38.5	3198	US-08-842-306B-48	Sequence 48, Appl
45	57.8	38.5	3198	US-08-838-973B-48	Sequence 48, Appl

ALIGNMENTS

RESULT 1
US-08-967-101-121/c
Sequence 121, Application US/08967101
Patent No. 5840540
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-967-101-121
Query Match 46.5%; Score 69.8; DB 2; Length 793;
Best Local Similarity 82.5%; Pred. No. 1.2e-15;
Matches 80; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
39 GCGCGCATGACGTGGATGCCCGGCGCGCATGATGATCAAGCTTATCGATCCG 98
|| ||| | | |||||||||||||||||||||||||||||||||||||||||||||

Query Match	46.58;	Score 69.8;	DB 4;	Length 793;
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Sequence 33, APPLICATION US/09111111
Patent No. 6436409

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; GENERAL INFORMATION:
; APPLICANT: GICOUEL, BRIGITTE
; APPLICANT: BERTHEU, FRANCOIS-XAVIER
; APPLICANT: ANDERSEN, PETER
; APPLICANT: RASMUSSEN, PETER B
; TITLE OF INVENTION: POLYNUCLEOTIDE FUNCTIONALLY CODING FOR THE LHP PROTEIN FROM MYCOE
; TITLE OF INVENTION: TUBERCULOSIS, ITS BIOLOGICALLY ACTIVE DERIVATIVE FRAGMENTS, AS W
; TITLE OF INVENTION: USING THE SAME
; FILE REFERENCE: 0660-0137-27X
; CURRENT APPLICATION NUMBER: US/09/116,492A
; CURRENT FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 60/252,631
; PRIOR FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: multiple cloning site-artificial DNA
US-09-116-492A-39

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Query Match          46.0%; Score 69; DB 4; Length 229;
Best Local Similarity 88.2%; Pred. No. 1.5e-15;
Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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QY 51 GTGATATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
    |||||||
Db 140 GTGATATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 81

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QY 111 GGGGGCCTACTACTACTATTTGTT 135
    |||||||
Db 80 GGGGGCCCGGTACCACTTTTGT 56

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```

RESULT 8
US-09-323-872A-26/C
; Sequence 26, Application US/09323872A
; Patent No. 6395539
; GENERAL INFORMATION:
; APPLICANT: Coschigano, Peter
; TITLE OF INVENTION: Compositions and Methods for Bioremediation
; FILE REFERENCE: OHU-03640
; CURRENT APPLICATION NUMBER: US/09/323,872A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/072,433
; PRIOR FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 147
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(147)
US-09-323-872A-26

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```

Query Match          44.7%; Score 67; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 6.6e-15;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 51 GTGATATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
    |||||||
Db 106 GTGATATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 47

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QY 111 GGGGGCC 117
    |||||||
Db 46 GGGGGCC 40

```

RESULT 9

```

US-09-643-597-306
; Sequence 306, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 306
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-643-597-306

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```

Query Match          44.7%; Score 67; DB 4; Length 457;
Best Local Similarity 100.0%; Pred. No. 9.7e-15;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 51 GTGATATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
    |||||||
Db 360 GTGATATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 419

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QY 111 GGGGGCC 117
    |||||||
Db 420 GGGGGCC 426

```

```

RESULT 10
US-08-976-259-108/C
; Sequence 108, Application US/08976259
; Patent No. 6316609
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Choi, Gil H.
; APPLICANT: Welch, Rodney A.
; TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli
; Patent No. 6316609
; NUMBER OF SEQUENCES: 142
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,259
; FILING DATE: Herewith
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,626 AND US 60/061,953
; ATTORNEY/AGENT INFORMATION:
; NAME: Steife, Eric K.
; REGISTRATION NUMBER: 36,688

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REFERENCE/DOCKET NUMBER: 1488.0740002/EKS/CEM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-976-259-108

Query Match
Best Local Similarity 44.7%; Score 67; DB 4; Length 752;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GTGATCCCCGGGCTGCAGGATTCGATTCAGCTTATCAGCTTACCGTGCAGG 110
DB 72 GTGATCCCCGGGCTGCAGGATTCGATTCAGCTTATCAGCTTACCGTGCAGG 13
QY 111 GGGGGCC 117
DB 12 GGGGGCC 6

RESULT 11
US-09-123-912-91
Sequence 91, Application US/09123912A
Patent No. 6312695
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
FILE REFERENCE: 210121.455C1
CURRENT APPLICATION NUMBER: US/09/123,912A
PRIORITY FILING DATE: 1998-07-27
PRIORITY FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 91
LENGTH: 858
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified_base
LOCATION: (570)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (591)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (655)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (664)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (667)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (683)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (711)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (739)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (760)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
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LOCATION: (765)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (777)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (787)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (792)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (794)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (801)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (804)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (809)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (817)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (820)
OTHER INFORMATION: Where n is a, c, g or t
US-09-123-912-91

Query Match
Best Local Similarity 44.7%; Score 67; DB 4; Length 858;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GTGATCCCCGGGCTGCAGGATTCGATTCAGCTTATCAGCTTACCGTGCAGG 110
DB 357 GTGATCCCCGGGCTGCAGGATTCGATTCAGCTTATCAGCTTACCGTGCAGG 416
QY 111 GGGGGCC 117
DB 417 GGGGGCC 423

RESULT 12
US-09-643-597-91
Sequence 91, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
PRIORITY FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 91
LENGTH: 858
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
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LOCATION: (1)...(858)
OTHER INFORMATION: n = A,T,C or G
US-09-643-597-91

Query Match 44.7%; Score 67; DB 4; Length 856;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GTGATCCCGGGGCTGAGAAATTCATATCACTTATCCATACCGTCGACCTCGAGG 110
|||||
DB 357 GTGATCCCGGGGCTGAGAAATTCATATCACTTATCCATACCGTCGACCTCGAGG 416
QY 111 GGGGGCC 117
|||||
DB 417 GGGGGCC 423

RESULT 13

US-08-446-935-6/c
Sequence 6, Application US/08446935
Patent No. 6187991
GENERAL INFORMATION:
APPLICANT: Soeller, Walter C.
APPLICANT: Carty, Maynard D.
APPLICANT: Kreutler, David K.
TITLE OF INVENTION: TRANSGENIC ANIMAL MODELS FOR TYPE II
TITLE OF INVENTION: DIABETES MELLITUS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pfizer Inc.
STREET: 235 East 42nd Street, 20th Floor
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10017-5755
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,935
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sheyka, Robert F.
REGISTRATION NUMBER: 31,304
REFERENCE/DOCKET NUMBER: PC8153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)573-1189
TELEFAX: (212)573-1939
TELEX: N/A
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2961 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
US-08-446-935-6

Query Match 44.7%; Score 67; DB 4; Length 2961;
Best Local Similarity 100.0%; Pred. No. 1.8e-14;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GTGATCCCGGGGCTGAGAAATTCATATCACTTATCCATACCGTCGACCTCGAGG 110
|||||
DB 726 GTGATCCCGGGGCTGAGAAATTCATATCACTTATCCATACCGTCGACCTCGAGG 667
QY 111 GGGGGCC 117
|||||
DB 666 GGGGGCC 660

RESULT 14

US-08-992-334-1/c
Sequence 1, Application US/08992334
Patent No. 5919678
GENERAL INFORMATION:
APPLICANT: Gruss, Alexandra
APPLICANT: Maguin, Emmanuelle
TITLE OF INVENTION: METHODS FOR USING A TEMPERATURE-SENSITIVE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christie Parker & Hale, LLP
STREET: 350 West Colorado Boulevard, Suite 500
CITY: Pasadena
STATE: California
COUNTRY: United States
ZIP: 91105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/992,334
FILING DATE: 17-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,752
FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00248
FILING DATE: 12-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 992/03034
FILING DATE: 13-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Prout, D. Bruce
REGISTRATION NUMBER: 20958
REFERENCE/DOCKET NUMBER: C93:31779
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 795-9900
TELEFAX: (626) 577-8800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3792 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: NO
ANTI-SENSE: YES
IMMEDIATE SOURCE:
CLONE: pg+host4
US-08-992-334-1

Query Match 44.7%; Score 67; DB 2; Length 3792;
Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GTGATCCCGGGGCTGAGAAATTCATATCACTTATCCATACCGTCGACCTCGAGG 110
|||||
DB 3541 GTGATCCCGGGGCTGAGAAATTCATATCACTTATCCATACCGTCGACCTCGAGG 3482
QY 111 GGGGGCC 117
|||||
DB 3481 GGGGGCC 3475

RESULT 15

US-08-302-752-1/c
Sequence 1, Application US/08302752
Patent No. 6025190


```
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THERMOSENSIBLE PLASMID
; NUMBER OF SEQUENCES: 3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,752
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9203034
; FILING DATE: 13-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR/93/00248
; FILING DATE: 12-MAR-1993
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3792 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-302-752-1

Query Match      44.7%; Score 67; DB 3; Length 3792;
Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  51 GTGATCCCCCGGGCTGCAGATTGATCAAGCTATACGATACCGTCGACCTCGAGG 110
    |||||||
Db  3541 GTGATCCCCCGGGCTGCAGATTGATCAAGCTATACGATACCGTCGACCTCGAGG 110
    |||||||
QY  111 GGGGGCC 117
    |||||||
Db  3481 GGGGGCC 3475
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Search completed: November 10, 2002, 08:36:21
Job time : 39.4558 secs

